

GenCore version 5.1.4.p5_4578
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 19, 2003, 22:09:49 ; Search time 1912 Seconds
(without alignments)
197.875 Million cell updates/sec

Title: US-09-768-840-1_COPY_254_266
Perfect score: 70
Sequence: 1 DLNKGCHLDGSEV 13

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-O=/cpn2.1/USPTO.spool/US09768840/runat_14052003_095711_16644/app_query.fasta_1.199
-DB=GenEmbl -QFMT=fastcap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -NORM=ext -HSPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-OUTFMT=ptc -NORM=ext -HSPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09768840.ecgn_1.1.2496.grunat_14052003_095711_16644 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_in:*
18: em_in:*
19: em_mu:*
20: em_mu:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_pl:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_fod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sv:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	70	100.0	1055	6	AR035969	Sequence
2	70	100.0	1055	6	AR135029	Sequence
3	70	100.0	1454	9	AF183423	Homo sapi
4	70	100.0	1463	6	AR083085	Sequence
5	70	100.0	1463	6	AR152960	Sequence
6	70	100.0	1470	9	BC011346	Homo sapi
7	70	100.0	1503	6	AX464230	Sequence
8	70	100.0	1507	6	AX354366	Sequence
9	70	100.0	1507	6	AX354369	Sequence
10	70	100.0	179394	9	AC010619	Homo sapi
11	62	88.6	1414	10	BC005487	Mus muscu
12	62	88.6	1421	10	BC025602	Mus muscu
13	62	88.6	110000	2	AC073763	Mus muscu
14	62	88.6	186243	2	AC073740	Mus muscu
15	62	88.6	191713	2	AC126256	Mus muscu
16	51	72.9	184443	2	AC114853	Rattus no
17	48	68.6	1454	9	BC010120	Homo sapi
18	48	68.6	1637	6	AX460089	Sequence
19	48	68.6	1832	6	AX480897	Sequence
20	48	68.6	1929	6	AX338084	Sequence
21	48	68.6	1998	10	MUSRCAL	Mus musculu
22	48	68.6	2089	9	BC001656	Homo sapi
23	48	68.6	2104	6	AX330466	Sequence
24	48	68.6	2104	9	HUMRCN	Human mRNa
25	48	68.6	2416	9	AK094360	Homo sapi
26	48	68.6	2557	10	MUSRET15	Mouse gene
27	48	68.6	2857	9	AK054901	Homo sapi
28	48	68.6	3430	6	AX405585	Sequence
29	48	68.6	44882	2	AC020850	Continuation (5 of
30	48	68.6	79018	9	AL627107	Human DNA
31	48	68.6	86986	2	AC112629	Rattus no
32	48	68.6	89311	2	AC097427	Rattus no
33	48	68.6	94497	9	HSDJ65P5	Human DNA
34	48	68.6	110000	2	AC020850	Continuation (3 of
35	48	68.6	134078	2	AC112459	Rattus no
36	48	68.6	137393	2	AC120265	Rattus no
37	48	68.6	149041	9	AC044782	Homo sapi
38	48	68.6	151955	2	AC097101	Rattus no
39	48	68.6	153448	2	AC112088	Rattus no
40	48	68.6	153567	2	AC111970	Rattus no
41	48	68.6	154241	2	AC128803	Rattus no
42	48	68.6	157392	2	AC120934	Rattus no
43	48	68.6	157639	2	AC131464	Rattus no
44	48	68.6	176708	2	AC027548	Homo sapi
45	48	68.6	179789	9	AC069543	Homo sapi

ALIGNMENTS

RESULT 1

AR035969
LOCUS AR035969 1055 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5871970.
ACCESSION AR035969
VERSION AR035969.1 GI:5952637
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1055)
AUTHORS Hillman,J.L. and Goli,S.K.
TITLE Calcium-binding protein
JOURNAL Patent: US 5871970-A 2 16-FEB-1999;
FEATURES Location/Qualifiers
source
1..1055
/organism="unknown"
BASE COUNT 225 a 300 c 375 g 151 t 4 others
ORIGIN
Alignment Scores: Length: 1055
Pred. No.: 0.0011 Matches: 13
Score: 70.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-768-840-1_COPY_254_266 (1-13) x AR035969 (1-1055)
Qy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 793 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 831
RESULT 2
AR135029
LOCUS AR135029 1055 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6194385.
ACCESSION AR135029
VERSION AR135029.1 GI:14123934
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1055)
AUTHORS Hillman,J.L. and Goli,S.K.
TITLE Calcium-binding protein
JOURNAL Patent: US 6194385-A 2 27-FEB-2001;
FEATURES Location/Qualifiers
source
1..1055
/organism="unknown"
BASE COUNT 225 a 300 c 375 g 151 t 4 others
ORIGIN
Alignment Scores: Length: 1055
Pred. No.: 0.0011 Matches: 13
Score: 70.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-768-840-1_COPY_254_266 (1-13) x AR135029 (1-1055)
Qy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 793 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 831
RESULT 3
AF183423
LOCUS AF183423 1454 bp mRNA linear PRI 02-SEP-2000
DEFINITION Homo sapiens reticulocabin precursor mRNA, complete cds.
ACCESSION AF183423
VERSION AF183423.1 GI:9963784

KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1454)
AUTHORS Peng,Y., Gu,Y., Huang,C., Xu,S., Han,Z., Fu,G. and Chen,Z.
TITLE A novel gene expressed in human hypothalamus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1454)
AUTHORS Peng,Y., Gu,W., Huang,C., Xu,S., Han,Z., Fu,G. and Chen,Z.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1999) Chinese National Human Genome Center at
Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
Shanghai 201203, P. R. China
FEATURES Location/Qualifiers
source
1..1454
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="hypothalamus"
33..1019
/note="HRP-iso"
/codon_start=1
/evidence=not_experimental
/product="reticulocabin precursor"
/protein_id="AAG09692.1"
/db_xref="GI:9963785"
/translation="MMWRPVSLLLLLLHGAQGRKPSDAGPHGQGRVHQAAPLSDAP
HDDAHNGFOYDHEAFLEGRVAKFQDLTPESQARLGGIVDRMDRAGSDGVVSLAEL
RAWIAHQOHRIRDSVSAWMDYDTRDGRGVGWEELRNATYGHYAPGEFHDVEADAET
YKMLARDERFRVADQDCDSMTREELTAFLHPEEPHMRDIVIAETLEDIDRKNKG
YVQVEYIADLYSAEPGEPPAWQTERQQFRDRLKDKGHLDSGEVGHVWLPVPAQD
QPLVEANHLHESDTRDKGRLSKAELGNMNVGSGATNYGEDLTRHDEL"
BASE COUNT 314 a 454 c 467 g 219 t
ORIGIN
Alignment Scores: Length: 1454
Pred. No.: 0.0015 Matches: 13
Score: 70.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-768-840-1_COPY_254_266 (1-13) x AF183423 (1-1454)
Qy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 792 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 830
RESULT 4
AR083085
LOCUS AR083085 1463 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 2 from patent US 5976801.
ACCESSION AR083085
VERSION AR083085.1 GI:10009875
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1463)
AUTHORS Bandman,O., Hillman,J.L., Lal,P., Corley,N.C. and Shah,P.
TITLE Human reticulocabin isoforms
JOURNAL Patent: US 5976801-A 2 02-NOV-1999;
FEATURES Location/Qualifiers
source
1..1463
/organism="unknown"
BASE COUNT 310 a 459 c 478 g 215 t 1 others
ORIGIN
Alignment Scores: Length: 1463
Pred. No.: 0.00156 Matches: 13
Score: 70.00


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ORIGIN
Alignment Scores:
Pred. No.: 0.0016 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AX464230 (1-1503)
QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 794 GATCTGAACAAGGATGGGACCTGGATGGAGTGAGGTG 832

RESULT 8
AX354366
LOCUS AX354366 1507 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 12 from Patent WO0196523.
ACCESSION AX354366
VERSION AX354366.1 GI:18619208
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Kennedy,G.C., Kang,S., Reinhard,C. and Jefferson,A.B.
AUTHORS Polynucleotides related to colon cancer
TITLE Patent: WO 0196523-A 12 20-DEC-2001;
JOURNAL CHIRON CORPORATION (US)
FEATURES
source
1. .1507
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 350 a 456 c 479 g 213 t 9 others
ORIGIN
Alignment Scores:
Pred. No.: 0.0016 Length: 1507
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AX354366 (1-1507)
QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 813 GATCTGAACAAGGATGGGACCTGGATGGAGTGAGGTG 851

RESULT 9
AX354369
LOCUS AX354369 1507 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 15 from Patent WO0196523.
ACCESSION AX354369
VERSION AX354369.1 GI:18619211
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Kennedy,G.C., Kang,S., Reinhard,C. and Jefferson,A.B.
AUTHORS Polynucleotides related to colon cancer
TITLE Patent: WO 0196523-A 15 20-DEC-2001;
JOURNAL CHIRON CORPORATION (US)
FEATURES
source
1. .1507
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 350 a 456 c 479 g 213 t 9 others
ORIGIN
Alignment Scores:
Pred. No.: 0.0016 Length: 1507
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AX354366 (1-1507)
QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 813 GATCTGAACAAGGATGGGACCTGGATGGAGTGAGGTG 851

RESULT 10
AX354369
LOCUS AX354369 179394 bp DNA linear PRI 29-MAY-2002
DEFINITION Homo sapiens chromosome 19 clone CTD-3148I10, complete sequence.
ACCESSION AC010619
VERSION AC010619.7 GI:21240682
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 179394)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 179394)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (16-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 179394)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On May 29, 2002 this sequence version replaced gi:15920094.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.4.
FEATURES
source
1. .179394
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="CTD-3148I10"
BASE COUNT 40992 a 48084 c 48579 g 41739 t
ORIGIN
Alignment Scores:
Pred. No.: 0.267 Length: 179394
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AC010619 (1-179394)
QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 129804 GATCTGAACAAGGATGGGACCTGGATGGAGTGAGGTG 129842

RESULT 11
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DB	721	GATCTGACAAAGGACGGCGCAACTGGATGGCAGTGAAGTC	759
RESULT 12			
BC025602			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REMARK			
COMMENT			

Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S.,
Dietch, N.L., Granite, S., Guan, X., Gupta, J., Haqhighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, O. L., Mastello, C., Maskari, B., Mastrian, S. D., McCloskey, J. C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P. J., Touchman, J. W., Tsurgeon, C., Vogt, J. L., Walker, M. A., Wetherby, K. D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E. D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 56 Row: b Column: 12

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction, Similarity but not identity

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FEATURES
source
to protein.
Location/Qualifiers
1. .1421.
/organism="Mus musculus"
/db_xref="taxon:10090"
/map="C57BL/6J"
/clone="MGC:36253 IMAGE:5250505"
/tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"

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/codon_start=1
/product="similar to hypothetical protein LOC57333"
/protein_id="AAH25602.1"
/db_xref="GI:19343898"
/translation="MMWRWSFLLLLLLRHWALKPSDPAGPHGQDRVHGHTPLSEAP
HDDAHGNQYDHEAFLGRDVAKEFDKLPESQARLGRIVDRDLGADSGQWYSLAE
L RAAWTAQOIRHFRSVSNAWHTYDTDRDGRVGEELRNATYGHTEPEEEDHVEDAE
TKKMLARDERFRVADQGSMSATREELATLHPPEEPMHRDVIVAATELBDLQNKDG
YQVVEYIADLYSEEPGEAPWQTEQQQFRFRDLNKGDLQDGSVGYWVLPSPQD
QPLVEANHLHLESHTDDKGRLSKAELISNNMFEVGSQATNYGEDLTRHDEL"
335 a 414 c 427 g 245 t

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Alignment Scores: 0.0452 Length: 1421
Pred. No.: 62.00 Matches: 12
Score: 92.31% Conservative: 1
Best Local Similarity: 92.31% Mismatches: 0
Query Match: 88.57% Indels: 0
DB: 10 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x BC025602 (1-1421)

QY 1 AspLeuAsnlyAspGlyHisLeuAspGlySerGluVal 13
Db 835 GATCTGACAGGACGGCACTGATGGATGGATGTC 873

RESULT 13
AC073763_0
WPCOMMENT

Sequence split into 4 fragments LOCUS AC073763 Accession AC073763

Fragment Name Begin End
AC073763_0 1 110000
AC073763_1 100001 210000
AC073763_2 200001 310000
AC073763_3 300001 409770

LOCUS AC073763 409770 bp DNA linear HTG 29-JUN-2000
DEFINITION Mus musculus clone RP23-343P5, WORKING DRAFT SEQUENCE, 63 unordered
pieces.

ACCESSION AC073763
VERSION AC073763.1 GI:8810380
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 409770)
TITLE DOE Joint Genome Institute.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 409770)
TITLE Direct Submission
JOURNAL DOE Joint Genome Institute.
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1868949
Center clone name: RPCI-23_343P5

Summary Statistics
Consensus quality: 353352 bases at least Q40
Consensus quality: 382147 bases at least Q30
Consensus quality: 388243 bases at least Q20
Estimated insert size: 217190; agarose-fp estimation
Quality coverage: 403570; sum-of-contigs estimation
Quality coverage: 8.5 in Q20 bases; agarose-fp estimation
Quality coverage: 4.57 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 63 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1003: contig of 1003 bp in length
1004 1103: gap of unknown length
1104 2382: contig of 1279 bp in length
2383 2482: gap of unknown length
2483 3614: contig of 1132 bp in length

3615 3714: gap of unknown length
3715 4723: contig of 1009 bp in length
4724 4824: gap of unknown length
4825 6292: contig of 1469 bp in length
6293 6393: gap of unknown length
6394 7431: contig of 1039 bp in length
7432 7531: gap of unknown length
7532 8869: contig of 1338 bp in length
8870 8969: gap of unknown length
8970 10066: contig of 1097 bp in length
10067 10166: gap of unknown length
10167 11248: contig of 1082 bp in length
11249 11349: contig of 1993 bp in length
11350 13341: gap of unknown length
13342 14589: contig of 1148 bp in length
14590 14689: gap of unknown length
14690 15797: contig of 1108 bp in length
15798 15897: gap of unknown length
15899 16915: contig of 1018 bp in length
16916 17015: gap of unknown length
17016 18367: contig of 1352 bp in length
18368 18467: gap of unknown length
18468 19731: contig of 1264 bp in length
19732 19831: gap of unknown length
19832 20934: contig of 1103 bp in length
20935 21034: gap of unknown length
21035 22801: contig of 1767 bp in length
22802 22901: gap of unknown length
22903 24724: contig of 1822 bp in length
24725 26095: contig of 1272 bp in length
26096 26195: gap of unknown length
26196 27347: contig of 1152 bp in length
27348 27447: gap of unknown length
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29638 31064: contig of 1426 bp in length
31065 31164: gap of unknown length
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33364 33463: gap of unknown length
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36041 36140: gap of unknown length
36141 38979: contig of 2839 bp in length
38980 39079: gap of unknown length
39080 42217: contig of 3138 bp in length
42218 42317: gap of unknown length
42318 44053: contig of 1736 bp in length
44054 44153: gap of unknown length
44154 45760: contig of 1607 bp in length
45761 45860: gap of unknown length
45861 48398: contig of 2538 bp in length
48399 48498: gap of unknown length
48499 52535: contig of 4037 bp in length
52536 52635: gap of unknown length
52636 56329: contig of 3694 bp in length
56330 60237: contig of 3828 bp in length
60238 60357: gap of unknown length
60358 63458: contig of 3101 bp in length
63459 63558: gap of unknown length
63559 66742: contig of 3184 bp in length
66743 66842: gap of unknown length
66843 69475: contig of 2633 bp in length
69476 73406: contig of 3831 bp in length
73407 73506: gap of unknown length
73507 77765: contig of 4259 bp in length
77766 77865: gap of unknown length
77866 82517: contig of 4651 bp in length
82518 82617: gap of unknown length
82619 88123: contig of 5507 bp in length
88124 88223: gap of unknown length


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* 88224 93473: contig of 5250 bp in length
* 93474 93573: gap of unknown length
* 93574 98553: contig of 5080 bp in length
* 98554 98753: gap of unknown length
* 98754 103469: contig of 4716 bp in length
* 103470 103569: gap of unknown length
* 103570 109147: contig of 5578 bp in length
* 109148 109247: gap of unknown length
* 109248 116537: contig of 7290 bp in length
* 116538 116637: gap of unknown length
* 116638 124186: contig of 7549 bp in length
* 124187 124286: gap of unknown length
* 124287 132204: contig of 7918 bp in length
* 132205 132304: gap of unknown length
* 132305 140886: contig of 8582 bp in length
* 140887 140986: gap of unknown length
* 140987 151063: contig of 10075 bp in length
* 151062 151161: gap of unknown length
* 151162 159241: contig of 8080 bp in length
* 159242 159341: gap of unknown length
* 159342 167120: contig of 7779 bp in length
* 167121 167220: gap of unknown length
* 167221 178631: contig of 11411 bp in length
* 178632 178731: gap of unknown length
* 178732 180111: contig of 11380 bp in length
* 180112 190211: gap of unknown length
* 190212 201488: contig of 11277 bp in length
* 201489 201588: gap of unknown length
* 201589 212958: contig of 11370 bp in length
* 212959 213058: gap of unknown length
* 213059 227047: contig of 13989 bp in length
* 227048 227147: gap of unknown length
* 227148 241205: contig of 14058 bp in length
* 241206 258822: contig of 17517 bp in length
* 258823 258922: gap of unknown length
* 258923 277262: contig of 18340 bp in length
* 277263 277362: gap of unknown length
* 277363 299258: contig of 21896 bp in length
* 299259 299358: gap of unknown length
* 299359 321207: contig of 21849 bp in length
* 321208 342521: contig of 21214 bp in length
* 342522 342621: gap of unknown length
* 342622 374406: contig of 31785 bp in length
* 374407 374506: gap of unknown length
* 374507 409770: contig of 35264 bp in length.

```

FEATURES

source

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1. .409770
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-343P5"
/clone_lib="RPCI mouse BAC library 23"

```

```

BASE COUNT 98446 a 106220 c 104553 g 94328 t 6223 others
ORIGIN

```

Alignment Scores:

```

Pred. No.: 4.73 Length: 110000
Score: 62.00 Matches: 12
Percent Similarity: 92.31% Conservative: 0
Best Local Similarity: 92.31% Mismatches: 1
Query Match: 88.57% Indels: 0
DB: 2 Gaps: 0

```

```

US-09-768-840-1_COPY_254_266 (1-13) x AC073763_0 (1-110000)

```

```

QY 1 AspleuAnLysAspGlyHisLeuAspGlySerGluVal 13

```

```

DB 65874 GATCTGAACNAGGCGGCGACTGCGATGCGAGTC 65912

```

RESULT 14

AC073740

LOCUS

186243 bp

DNA

linear

HTG 18-JUL-2000

BASE COUNT

43755 a 47751 c 48436 g 45300 t 1001 others

DEFINITION

```

Mus musculus clone RP23-274I22, WORKING DRAFT SEQUENCE, 11 ordered
pieces.

```

ACCESSION

AC073740

VERSION

AC073740.2 GI:9256778

KEYWORDS

HTG; HTGS_PHASE2; HTGS_DRAFT.

SOURCE

Mus musculus.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

DOE Joint Genome Institute.

Sequencing of Mouse

Unpublished

DOE Joint Genome Institute.

Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Jul 18, 2000 this sequence version replaced gi:8610357.

-----Genome Center

Center: Joint Genome Institute

Center Code: JGI

Web site: http://www.jgi.doe.gov

Project Information

Center Project Name: 1842302

Center clone name: RPCI-23-274I22

Summary Statistics

Consensus quality: 175948 bases at least Q40

Consensus quality: 182693 bases at least Q30

Consensus quality: 184188 bases at least Q20

Estimated insert size: 202290; agarose-fp estimation

Estimated insert size: 185793; sum-of-contigs estimation

Quality coverage: 6.58 in Q20 bases; agarose-fp estimation

Quality coverage: 7.17 in Q20 bases; sum-of-contigs estimation

NOTE: This is a 'working draft' sequence. It currently

consists of 11 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces

is believed to be correct as given, however the sizes

of the gaps between them are based on estimates that have

been provided by the submitter

This sequence will be replaced

by the finished sequence as soon as it is available and

the accession number will be preserved.

1 439 538: contig of 438 bp in length

439 538: gap of unknown length

12617 12716: contig of 12078 bp in length

12617 12716: gap of unknown length

12717 24949: contig of 12233 bp in length

12717 24949: gap of unknown length

24950 25050: contig of 17568 bp in length

24950 25050: gap of unknown length

42618 42717: gap of unknown length

42618 42717: gap of unknown length

92551 92650: contig of 49833 bp in length

92551 92650: gap of unknown length

92651 94922: contig of 2272 bp in length

92651 94922: gap of unknown length

94923 95023: contig of 1998 bp in length

94923 95023: gap of unknown length

95023 97021: contig of 59952 bp in length

95023 97021: gap of unknown length

97021 157072: contig of 174862 bp in length

97021 157072: gap of unknown length

157073 174863: contig of 17690 bp in length

157073 174863: gap of unknown length

174863 174963: contig of 3478 bp in length

174863 174963: gap of unknown length

174963 178441: contig of 7703 bp in length.

178441 178541: contig of 7703 bp in length.

178541 186243: contig of 7703 bp in length.

186243 186243: contig of 7703 bp in length.

Location/Qualifiers

1. .186243

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="RP23-274I22"

/clone_lib="RPCI mouse BAC library 23"

Tue May 20 14:43:29 2003

us-09-768-840-1_copy_254_266.p2n.rge

ORIGIN

Alignment Scores: 8.3 Length: 186243
Pred. No.: 62.00 Matches: 12
Score: 92.31% Conservativity: 0
Percent Similarity: 92.31% Mismatches: 1
Best Local Similarity: 92.31% Indels: 0
Query Match: 88.57% Gaps: 0
DB: 2

US-09-768-840-1_COPY_254_266 (1-13) x AC073740 (1-186243)

QY 1 AspleuAsnlyspGlyHisLeuAspGlySerGluVal 13
|||||
Db 123065 GATCTGACACAGGACGGCGGACCTGGATGGCAGTGAAGTC 123103

RESULT 15

AC126256 191713 bp DNA linear HTG 05-JUL-2002
LOCUS Mus musculus chromosome UNK clone RP24-235B15, WORKING DRAFT
DEFINITION SEQUENCE, 5 unordered pieces.

ACCESSION AC126256.2 GI:21699708
VERSION HTG; HTGS_PRAISE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS house mouse.
SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 191713)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone

REFERENCE

AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 191713)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA

3 (bases 1 to 191713)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (05-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA

On Jul 5, 2002 this sequence version replaced gi:21693961.
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BB0235B15
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing method: plasmid; 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 189879 bases at least Q40
Consensus quality: 190172 bases at least Q30
Consensus quality: 190337 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 2693: contig of 2693 bp in length
* 2694 2793: gap of unknown length
* 2794 27767: contig of 24974 bp in length

* 27768 27867: gap of unknown length
* 27868 61313: contig of 33446 bp in length
* 61314 61413: gap of unknown length
* 61414 131828: contig of 70415 bp in length
* 131829 131928: gap of unknown length
* 131929 191713: contig of 59785 bp in length.

FEATURES

source Location/Qualifiers
1..191713
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP24-235B15"
1..2693
/note="assembly_name:Contig32"
misc_feature 2794..27767
/note="assembly_name:Contig33"
misc_feature 27868..61313
/note="assembly_name:Contig34"
misc_feature 61414..131828
/note="assembly_name:Contig35"
misc_feature 131929..191713
/note="assembly_name:Contig36"

BASE COUNT 46194 a 49474 c 49482 g 46163 t 400 others
ORIGIN

Alignment Scores:

Pred. No.: 8.56 Length: 191713
Score: 62.00 Matches: 12
Percent Similarity: 92.31% Conservativity: 0
Best Local Similarity: 92.31% Mismatches: 1
Query Match: 88.57% Indels: 0
DB: 2 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AC126256 (1-191713)

QY 1 AspleuAsnlyspGlyHisLeuAspGlySerGluVal 13
|||||

Db 161430 GATCTGACACAGGACGGCGGACCTGGATGGCAGTGAAGTC 161468

Search completed: May 20, 2003, 07:03:46
Job time : 1995 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: May 19, 2003, 12:24:06 ; Search time 233 seconds
(without alignments)
125.648 Million cell updates/sec

Title: US-09-768-840-1_COPY_254_266

Perfect score: 70

Sequence: 1 DLNKGCHLDGSEV 13

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q/cgn2_1/USPTO.spool/US09768840/runat_14052003_095710_16637/app_query.fasta_1.199
-DB=N_Geneseq_101002 -Qfmt=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09768840 -CGN_1_1_263 @runat_14052003_095710_16637 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002.*
1: /SIDS2/cgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS2/cgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS2/cgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS2/cgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS2/cgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS2/cgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS2/cgdata/geneseq/geneseq-emb1/NA1986.DAT.*
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9: /SIDS2/cgdata/geneseq/geneseq-emb1/NA1988.DAT.*
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12: /SIDS2/cgdata/geneseq/geneseq-emb1/NA1991.DAT.*
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15: /SIDS2/cgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS2/cgdata/geneseq/geneseq-emb1/NA1995.DAT.*
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23: /SIDS2/cgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/cgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	70	100.0	1055	19	AAV57600	Human calcium-bind
2	70	100.0	1055	22	AAH48279	Human calcium bind
3	70	100.0	1463	20	AAH47229	Human reticulocalb
4	70	100.0	1480	22	AAI63890	Human polynucleoti
5	70	100.0	1480	22	AAS31631	CDNA encoding nove
6	70	100.0	1480	23	ABK43732	DNA encoding novel
7	70	100.0	1487	22	ABK34992	Human colon cancer
8	70	100.0	1503	20	AAK52253	Protein PRO272 cDN
9	70	100.0	1503	21	AAC58589	Human PRO272 prote
10	70	100.0	1503	22	AAS21425	Human CDNA sequenc
11	70	100.0	1503	22	AAF72411	Human PRO272 CDNA
12	70	100.0	1503	22	AAC97455	Human anglogenesis
13	70	100.0	1507	20	AAK00656	Human secreted pro
14	70	100.0	1507	24	AAK41601	Human colon cancer
15	70	100.0	1507	24	AAK41603	Human colon cancer
16	70	100.0	1542	21	AAZ36246	CDNA encoding a bo
17	48	68.6	236	22	ABA64600	Human breast cell
18	48	68.6	236	22	ABA64600	Human foetal liver
19	48	68.6	236	22	ABA31726	Probe #10192 for g
20	48	68.6	236	22	AAK13040	Human brain expres
21	48	68.6	236	22	AAK38771	Human bone marrow
22	48	68.6	236	22	AAI19577	Probe #9510 for ge
23	48	68.6	236	22	AAI44770	Probe #13456 used
24	48	68.6	236	22	AAI05297	Probe #5288 used t
25	48	68.6	236	24	ABS12846	Human genome-deriv
26	48	68.6	476	22	ABA51941	Human foetal liver
27	48	68.6	476	22	ABA21756	Probe #222 for gen
28	48	68.6	476	22	AAK00229	Human brain expres
29	48	68.6	476	22	AAK25672	Human bone marrow
30	48	68.6	476	22	AAI10299	Probe #232 for gen
31	48	68.6	476	22	AAI13549	Probe #232 used to
32	48	68.6	476	22	AAI00235	Probe #226 used to
33	48	68.6	476	24	ABS00245	Human genome-deriv
34	48	68.6	686	24	ABK44106	CDNA #46 encoding
35	48	68.6	1386	22	AAI66981	Human membrane tra
36	48	68.6	1616	23	AAS86824	DNA encoding novel
37	48	68.6	1637	24	AAI72316	Human transporter
38	48	68.6	1929	22	AAI66980	Human membrane tra
39	48	68.6	2055	24	ABQ55036	Human ovarian anti
40	48	68.6	2104	24	ABK64404	Human benign prost
41	48	68.6	2104	24	ABL62638	Colon adenocarcino
42	48	68.6	2358	22	AAH72801	Human cervical can
43	48	68.6	2625	22	AAS44597	Human full-length
44	48	68.6	2644	22	AAS44769	Human contig polyn
45	48	68.6	3430	24	AAD36323	Human transporter

ALIGNMENTS

RESULT 1
AAV57600
ID AAV57600 standard; cDNA; 1055 BP.
AC AAV57600;
XX
XX
XX
DT 15-DEC-1998 (first entry)
XX
DE Human calcium-binding protein encoding cDNA.
XX Human; calcium-binding protein; reticulocalbin; sickle cell anaemia;
KW HCBP; beta thalassaemia; cell proliferation; cancer; adenocarcinoma;
KW leukemia; lymphoma; melanoma; sarcoma; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 34..1020

XX Bandman O, Corley NC, Hillman JL, Lal P, Shah P;
 PI WPI; 1999-180492/15.
 DR P-PSDB; AAY00916.
 XX
 PT New human reticulocalbin isoforms - useful to diagnose, prevent,
 PT and treat infectious, developmental, neoplastic, and immunological
 PT disorders
 XX
 PS Claim 7; Fig 1; 82pp; English.
 XX
 CC This sequence encodes the human reticulocalbin gamma (RCNgamma) of the
 CC invention. RCNgamma and RCNdelta are used to treat an infectious or
 CC developmental disorder, and antagonists of them are used to treat a
 CC neoplastic or immunological disorder. Infectious disorders include e.g.
 CC pneumonia, lymphocytic choriomeningitis, Hantavirus, chronic bronchitis,
 CC hepatitis, herpesviruses, yellow fever, influenza, cancer, measles,
 CC mumps, rhinovirus, poliovirus, coxsackie-virus, smallpox, Colorado tick
 CC fever, HIV, rabies, gastroenteritis, and rubella, encephalitis, and
 CC bacterial, fungal, parasitic, protozoal, or helminthic infections.
 CC Development disorders include e.g. renal tubular acidosis, anaemia,
 CC Cushing's syndrome, achondroplastic dwarfism, epilepsy, gonadal
 CC dysgenesis, hereditary neuropathies such as Charcot-Marie-Tooth disease,
 CC and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders
 CC such as Sydenham's chorea and cerebral palsy, spinal bifida, and
 CC congenital glaucoma, cataract, or sensorineural hearing loss. Neoplastic
 CC disorders include e.g. adenocarcinoma, leukaemia, lymphoma, melanoma,
 CC myeloma, sarcoma and teratocarcinoma. Overexpression of reticulocalbin
 CC mRNA has been associated with increased matrix invasion properties of
 CC three human breast cancer lines.
 XX
 SQ Sequence 1463 BP; 310 A; 459 C; 478 G; 215 T; 1 other;

Alignment Scores:
 Pred. No.: 0.00186 Length: 1463
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAX27229 (1-1463)

Oy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal I3
 |||||
 Db 808 GATCTGACACAGGATGGCACCCTGGATGGAGTGAGGTG 846

RESULT 4
 AAI63890
 ID AAI63890 standard; cDNA: 1480 BP.
 AC AAI63890;
 XX
 XX 22-OCT-2001 (first entry)
 DT
 XX
 XX Human polynucleotide SEQ ID NO 98.
 DE
 XX
 KW Human: antiarthritic; antirheumatic; antiproliferative; vasotropic;
 KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
 KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
 KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
 KW antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
 KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
 KW cardiovascular disorder; neurological disease; infection; human; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200155308-A2.
 PN
 XX
 PD 02-AUG-2001.
 XX
 XX 17-JAN-2001; 2001WO-US01309.

XX 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
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 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 23-AUG-2000; 2000US-0227182.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234937.
 PR 26-SEP-2000; 2000US-0234998.
 PR 27-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.

PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
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PR 08-NOV-2000; 2000US-0246528.
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PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PR (HUMA-) HUMAN GENOME SCI INC.
PR Rosen CA, Barash SC, Ruben SM;
PR WPI; 2001-488781/53.
PR P-PSDB; AAM43584.
PR New isolated nucleic acids and polypeptides, useful for diagnosing,

PT treating and/or preventing human diseases and disorders -
XX Claim 1; SEQ ID NO 98; 664pp + Sequence Listing; English.
XX The invention relates to human polynucleotides (AAI63803-AAI64012) and
CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 1480 BP; 329 A; 458 C; 479 G; 214 T; 0 other;

Alignment Scores:
Pred. No.: 0.00188 Length: 1480
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAI63890 (1-1480)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||
DB 806 GATCTGAACAAGATGGGCACCTGGACGGAGTGAGGTG 844

RESULT 5
AAS31631
ID AAS31631 standard; cDNA; 1480 BP.
XX AC AAS31631;
XX DT 04-DEC-2001 (first entry)
XX DE cDNA encoding novel human calcium-binding protein #55.
XX Human; calcium-binding protein; calcium flux; neurological disease;
KW Immune dysfunction; digestive disorder; neoplastic disease;
KW blood disorder; infectious disease; gene therapy; immunosuppressive;
KW antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
KW virucide; ss.
XX OS Homo sapiens.
XX PN WO200155304-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01302.
XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
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PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
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PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
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PR 12-SEP-2000; 2000US-0232968.
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PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
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PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
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PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
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PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
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PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
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PR 08-NOV-2000; 2000US-0246611.
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PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
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PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
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PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249266.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 05-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-02594097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465568/50.
DR P-PSDB; AAU19946.
XX
XX Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition -
PT Claim 4; SEQ ID No 65; 542pp; English.
XX
XX The present invention relates to the isolation of novel human
CC calcium-binding proteins (AAU1989; AAU1996), and cDNA and genomic
CC sequences encoding for these proteins. The sequences of the invention
CC are useful in the diagnosis, prevention and/or prognosis of diseases
CC associated with aberrant calcium flux. Such disorders include
CC neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
CC immune dysfunction (e.g. severe combined immunodeficiency, SCID),

CC digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
 CC disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
 CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
 CC novel calcium-binding proteins are also useful as screening tools to
 CC identify antagonists and/or agonists that may enhance or inhibit
 CC activities mediated by calcium-binding proteins. The polynucleotides of
 CC the invention are also useful in gene therapy. AAS31577-AAS31654
 CC represent cDNA sequences encoding for the novel human calcium-binding
 CC proteins.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1480 BP; 329 A; 458 C; 479 G; 214 T; 0 other;

Alignment Scores:
 Pred. No.: 0.00188 Length: 1480
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAS31631 (1-1480)

QY 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13
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 Db 806 GAICTGAACAAGATGGCGACCTGGACGGGAGTGAGGTG 844

RESULT 6

ABK43732
 ID ABK43732 standard; cDNA; 1480 BP.

AC ABK43732;

DT 05-JUN-2002 (first entry)

XX DNA encoding novel central nervous system protein #312.

XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;
 KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy; gene; ss.

XX Homo sapiens.

XX WO200155318-A2.

XX 03-AUG-2001.

XX 17-JAN-2001; 2001WO-US01332.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180828.

PR 24-FEB-2000; 2000US-0184564.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
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 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
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 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 21-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 13-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.

CC Additionally, N may be used to produce the colon cancer-associated Ps,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAB77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 SQ Sequence 1487 BP; 344 A; 452 G; 464 G; 221 T; 6 other;

Alignment Scores:
 Pred. No.: 0.00189 Length: 1487
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAH34992 (1-1487)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
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 Db 793 GATCTGACACAGGATGGGCACCTGGATGGAGTGAGGTG 831

RESULT 8

AAH52253
 ID AAX52253 standard; DNA; 1503 BP.
 XX
 AC AAX52253;
 XX
 XX
 DT 25-JUN-1999 (first entry)
 XX
 DE Protein PRO272 cDNA clone DNA40620-1183.
 XX

Secreted protein; transmembrane protein; human; enterocolitis;
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
 KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
 KW anti-thrombotic; wound healing; tissue repair; ss.
 KW
 OS Homo sapiens.
 XX
 XX
 PN W09914328-A2.
 XX
 XX
 PD 25-MAR-1999.
 XX
 XX
 PF 16-SEP-1998; 98WO-US19330.
 XX

25-NOV-1997; 97US-0066840.
 PR 17-SEP-1997; 97US-0059113.
 PR 17-SEP-1997; 97US-0059115.
 PR 17-SEP-1997; 97US-0059117.
 PR 17-SEP-1997; 97US-0059119.
 PR 17-SEP-1997; 97US-0059121.
 PR 17-SEP-1997; 97US-0059122.
 PR 17-SEP-1997; 97US-0059184.
 PR 18-SEP-1997; 97US-0059263.
 PR 18-SEP-1997; 97US-0059266.
 PR 15-OCT-1997; 97US-0062125.
 PR 17-OCT-1997; 97US-0062285.
 PR 17-OCT-1997; 97US-0062287.
 PR 21-OCT-1997; 97US-0063486.
 PR 24-OCT-1997; 97US-0062814.
 PR 24-OCT-1997; 97US-0062816.
 PR 24-OCT-1997; 97US-0063045.
 PR 24-OCT-1997; 97US-0063120.
 PR 24-OCT-1997; 97US-0063121.
 PR 24-OCT-1997; 97US-0063127.
 PR 24-OCT-1997; 97US-0063128.

PR 27-OCT-1997; 97US-0063329.
 PR 27-OCT-1997; 97US-0063327.
 PR 28-OCT-1997; 97US-0063541.
 PR 28-OCT-1997; 97US-0063542.
 PR 28-OCT-1997; 97US-0063544.
 PR 28-OCT-1997; 97US-0063549.
 PR 28-OCT-1997; 97US-0063550.
 PR 28-OCT-1997; 97US-0063564.
 PR 29-OCT-1997; 97US-0063435.
 PR 29-OCT-1997; 97US-0063704.
 PR 29-OCT-1997; 97US-0063732.
 PR 29-OCT-1997; 97US-0063738.
 PR 29-OCT-1997; 97US-0063734.
 PR 29-OCT-1997; 97US-0064215.
 PR 31-OCT-1997; 97US-0063735.
 PR 31-OCT-1997; 97US-0063870.
 PR 31-OCT-1997; 97US-0064103.
 PR 03-NOV-1997; 97US-0064248.
 PR 07-NOV-1997; 97US-0064809.
 PR 12-NOV-1997; 97US-0065186.
 PR 17-NOV-1997; 97US-0065846.
 PR 18-NOV-1997; 97US-0065893.
 PR 21-NOV-1997; 97US-0066120.
 PR 21-NOV-1997; 97US-0066364.
 PR 24-NOV-1997; 97US-0066772.
 PR 24-NOV-1997; 97US-0066466.
 PR 24-NOV-1997; 97US-0066770.
 PR 24-NOV-1997; 97US-0066511.
 PR 24-NOV-1997; 97US-0066453.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX
 PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
 XX
 XX WPI; 1999-229533/19.
 DR P-PSDB; AAY13382.
 DR
 XX New isolated human genes and polypeptides used in, e.g. treatment of
 XX gastrointestinal ulceration
 XX
 XX Claim 2; Fig 79; 320pp; English.
 XX
 CC AAX52213-74 encode secreted and transmembrane human proteins, and are
 CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
 CC fetal brain, fetal liver and fetal retina. The encoded polypeptides
 CC have specific uses based on their homology to known polypeptides,
 CC e.g. PRO211 and PRO217 can be used for disorders associated with the
 CC preservation and maintenance of gastrointestinal mucosa and the repair
 CC of acute and chronic mucosal lesions (e.g. enterocolitis,
 CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
 CC microvillus atrophy), skin diseases associated with abnormal
 CC keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as
 CC lung squamous cell carcinoma of the vulva and gliomas), potent effects on
 CC cell growth and development, diseases related to growth or survival of
 CC nerve cells including Parkinson's disease, Alzheimer's disease, ALS,
 CC neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for
 CC reducing dermal scarring. PRO264 can be used as a target for anti-tumor
 CC drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia
 CC areata. PRO269 can be used as an anti-thrombotic agent; PRO287
 CC polypeptides and portions may have therapeutic applications in wound
 CC healing and tissue repair; PRO317 can be used for treating problems of
 CC the kidney, uterus, endometrium, blood vessels, or related tissue, e.g.
 CC in the heart of genital tract.
 XX
 SQ Sequence 1503 BP; 357 A; 456 C; 474 G; 216 T; 0 other;

Alignment Scores:

Pred. No.: 0.00192 Length: 1503
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0


```

US-09-768-840-1_COPY_254_266 (1-13) x AAS52253 (1-1503)
QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
DB 794 GATCTGACACAGGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 9
AAC58589
ID AAC58589 standard; cDNA; 1503 BP.
XX
AC AAC58589;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO272 protein UNQ239 encoding cDNA SEQ ID NO:50.
XX
KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease; ss.
XX
OS Homo sapiens.
XX
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05841.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99US-0123618.
PR 12-MAR-1999; 99US-0123957.
PR 23-MAR-1999; 99US-0125775.
PR 12-APR-1999; 99US-0128849.
PR 20-APR-1999; 99WO-US08615.
PR 28-APR-1999; 99US-0131445.
PR 04-MAY-1999; 99US-0132371.
PR 14-MAY-1999; 99US-0134287.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.

06-JAN-2000; 2000WO-US00277.
06-JAN-2000; 2000WO-US00376.
11-FEB-2000; 2000WO-US03565.
18-FEB-2000; 2000WO-US04341.
18-FEB-2000; 2000WO-US04342.
22-FEB-2000; 2000WO-US04414.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RJ, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tamas D, Watanabe CK, Wood WI, Yan M;
XX
WPI: 2000-572271/53.
DR P-PSDB; AAB33424.
XX
PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus .
XX
PS Claim 23; Fig 21; 309pp; English.
XX
CC The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
CC autoimmune or immune-mediated skin diseases, allergic diseases,
CC immunological diseases of the lung, and transplantation associated
CC diseases including graft rejection and graft-versus-host-disease.
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 1503 BP; 357 A; 456 C; 474 G; 216 T; 0 other;

Alignment Scores:
Pred. No.: 0.00192 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAC58589 (1-1503)
QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
DB 794 GATCTGACACAGGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 10
AAS21425
ID AAS21425 standard; cDNA; 1503 BP.
XX
AC AAS21425;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human cDNA sequence encoding for PRO272 polypeptide.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.
XX

```


OS Homo sapiens.
XX WO200140466-A2.
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-US32678.
XX 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.
XX 02-DEC-1999; 99WO-US28551.
XX 02-DEC-1999; 99WO-US28564.
XX 02-DEC-1999; 99WO-US28565.
XX 09-DEC-1999; 99US-0170262.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30911.
XX 20-DEC-1999; 99WO-US30999.
XX 30-DEC-1999; 99WO-US31243.
XX 06-JAN-2000; 2000WO-US00277.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.
XX 18-FEB-2000; 2000WO-US04342.
XX 22-FEB-2000; 2000WO-US04414.
XX 24-FEB-2000; 2000WO-US04914.
XX 01-MAR-2000; 2000WO-US05004.
XX 20-MAR-2000; 2000WO-US05601.
XX 21-MAR-2000; 2000WO-US07377.
XX 30-MAR-2000; 2000WO-US07532.
XX 30-MAR-2000; 2000WO-US08439.
XX 17-MAY-2000; 2000WO-US13705.
XX 22-MAY-2000; 2000WO-US14042.
XX 30-MAY-2000; 2000WO-US14941.
XX 02-JUN-2000; 2000WO-US15264.
XX 10-NOV-2000; 2000WO-US30873.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
WPI; 2001-408281/43.
P-PSDB; AAU12353.

Isolated, secretory and transmembrane PRO polypeptide used to detect
other PRO polypeptides, link bioactive molecules to cells expressing
PRO polypeptides, and detect the presence of mammalian tumours e.g.
lung, breast, prostate, cervical

Claim 3; Fig 363; 813pp; English.

AA521244-AA521518 encode for novel human secretory and transmembrane
PRO polypeptides. The PRO polypeptides are useful to detect other
PRO polypeptides, to link bioactive molecules to cells expressing
PRO polypeptides, to modulate biological activities of cells expressing
PRO polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, rectal, cervical or liver tumours by comparing PRO
polypeptide expression in a cell sample to that in a control sample.
Some of the 275 sequences are also useful to stimulate the release of
tumour necrosis factor-alpha (TNF-alpha) from human blood, the
proliferation or differentiation of chondrocytes, the proliferation or
gene expression in pericyte cells, the release of proteoglycans from
cartilage, the proliferation of inner ear utricular supporting cells or
of T-lymphocytes, the release of a cytokine from peripheral blood
monocytes (PBMCs), or the proliferation of endothelial cells. Some of
the PRO polypeptides may modulate glucose or free fatty acid uptake by
skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
to factor VIIA. The PRO polypeptides can be used in assays to identify
molecules involved in binding interactions. The polynucleotides encoding
PRO polypeptides can be used to generate probes, antisense RNA/DNA,
transgenic or knock out animals and can be used in gene therapy.

SQ Sequence 1503 BP; 357 A; 456 C; 474 G; 216 T; 0 other;
Alignment Scores:
Pred. No.: 0.00192 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAS21425 (1-1503)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 794 GATCTGAACAAGGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 11

AAF72411
ID AAF72411 standard; cDNA; 1503 BP.

XX AC AAF72411;

XX DT 24-APR-2001 (first entry)

XX DE Human PRO272 cDNA.

XX KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
XX KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
XX KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
XX KW antiarthritic; antinfertility; antidiabetic; antiviral; diabetes;
XX KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
XX KW ischaemia; inflammation; ss.

XX OS Homo sapiens.

XX PN WO200104311-A1.

XX PD 18-JAN-2001.

XX PF 22-FEB-2000; 2000WO-US04414.

XX PR 07-JUL-1999; 99US-0143048.

XX PR 26-JUL-1999; 99US-0145698.

XX PR 28-JUL-1999; 99US-0146222.

XX PR 08-SEP-1999; 99WO-US20594.

XX PR 13-SEP-1999; 99WO-US20944.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 15-SEP-1999; 99WO-US21547.

XX PR 05-OCT-1999; 99WO-US23089.

XX PR 29-NOV-1999; 99WO-US28214.

XX PR 30-NOV-1999; 99WO-US28313.

XX PR 16-DEC-1999; 99WO-US30095.

XX PR 20-DEC-1999; 99WO-US30911.

XX PR 20-DEC-1999; 99WO-US30999.

XX PR 05-JAN-2000; 99WO-US00219.

XX (GETH) GENENTECH INC.

XX PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

XX PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

XX PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;

XX PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

XX PI Williams PM, Wood WI;

XX WPI; 2001-081051/09.

XX P-PSDB; AAB80250.

Sixty one nucleic acids encoding PRO polypeptides which are useful in
the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
squamous cell carcinoma) and neurodegenerative diseases (e.g.
Alzheimer's disease) -

Claim 2; Fig 79; 393pp; English.

XX The present sequence is one of sixty one nucleic acids encoding novel
 CC secreted and transmembrane PRO polypeptides. The PRO polypeptides are
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
 CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
 CC endometrial bleeding angiogenesis, ischaemias such as coronary
 CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
 CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
 CC diabetes and retinal disorders such as retinitis pigmentosum.
 CC The PRO nucleic acids have applications in molecular biology, including
 CC use as hybridization probes, and in chromosome and gene mapping.
 XX

Sequence 1503 BP; 357 A; 456 C; 474 G; 216 T; 0 other;

Alignment Scores:
 Pred. No.: 0.00192 Length: 1503
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAF72411 (1-1503)

QY 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13

Db 794 GATCTGAACAAGGATGGCCACCTGGATGGAGTGAGGTG 832

RESULT 12

AAC97455

ID AAC97455 standard; cDNA; 1503 BP.

AC AAC97455;

XX 28-FEB-2001 (first entry)

DE Human angiogenesis-associated protein PRO272 cDNA, SEQ ID NO:112.

XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal; ss.

OS Homo sapiens.

XX WO200053753-A2.

PN 14-SEP-2000.

PD 05-JAN-2000; 2000WO-US00219.

PF 08-MAR-1999; 99WO-US05028.

XX 12-MAR-1999; 99US-0123957.

PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 05-OCT-1999; 99WO-US23089.

PR 30-NOV-1999; 99WO-US28313.

PR 30-NOV-1999; 99WO-US28409.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

(GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Coddard A;
 XX Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MK, Marsters SA;
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;

XX WPI: 2001-090793/10.

DR P-PSDB; AAB53085.

XX New isolated nucleic acid for producing a PRO polypeptide, analyzing
 PT genetic disorders and treating cardiovascular, endothelial or
 PT angiogenic disorders, such as atherosclerosis, wounds or cancer -

XX Claim 58; Fig 43; 293pp; English.

XX The invention relates to novel human angiogenesis-associated proteins
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 CC PRO proteins. The invention also relates to vectors and host cells
 CC comprising a PRO nucleic acid, the recombinant production of a PRO
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
 CC compounds which inhibit the expression of a PRO gene. The invention
 CC additionally encompasses methods of identifying modulators of PRO
 CC expression or activity; diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting
 CC mutations in a PRO gene, or the expression level of a PRO gene within a
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 CC administration of a PRO protein, or an agonist or antagonist thereof.
 CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
 CC agonists and PRO antagonists may be used as therapeutic agents to treat
 CC cardiovascular, endothelial or angiogenic disorders, such as
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
 CC disease, or stroke. PRO nucleic acids are additionally useful in the
 CC recombinant production of PRO proteins, as hybridisation probes to
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,
 CC to map genes encoding PRO proteins, to analyse genetic disorders, and in
 CC gene therapy. PRO nucleic acids can also be used to produce transgenic
 CC animals useful for the development and screening of potential
 CC therapeutic agents. The present sequence represents a cDNA encoding a PRO
 CC protein of the invention.

XX Sequence 1503 BP; 357 A; 456 C; 474 G; 216 T; 0 other;

Alignment Scores:

Pred. No.: 0.00192 Length: 1503
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAC97455 (1-1503)

QY 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13

Db 794 GATCTGAACAAGGATGGCCACCTGGATGGAGTGAGGTG 832

RESULT 13

AAX00656

ID AAX00656 standard; DNA; 1507 BP.

XX AAX00656;

XX 25-MAR-1999 (first entry)

XX Human secreted protein gene 46 clone HSJBQ79.

DE

XX

KW	Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX	
OS	Homo sapiens.
XX	
XX	WO9842738-A1.
PN	
XX	
PD	01-OCT-1998.
XX	
PF	19-MAR-1998; 98WO-US05311.
XX	
30-MAY-1997;	97US-0050937.
PR	21-MAR-1997; 97US-0041276.
PR	21-MAR-1997; 97US-0041277.
PR	21-MAR-1997; 97US-0041281.
PR	21-MAR-1997; 97US-0042344.
PR	30-MAY-1997; 97US-0048069.
PR	30-MAY-1997; 97US-0048094.
PR	30-MAY-1997; 97US-0048095.
PR	30-MAY-1997; 97US-0048096.
PR	30-MAY-1997; 97US-0048099.
PR	30-MAY-1997; 97US-0048131.
PR	30-MAY-1997; 97US-0048135.
PR	30-MAY-1997; 97US-0048154.
PR	30-MAY-1997; 97US-0048160.
PR	30-MAY-1997; 97US-0048186.
PR	30-MAY-1997; 97US-0048187.
PR	30-MAY-1997; 97US-0048188.
PR	30-MAY-1997; 97US-0048350.
PR	30-MAY-1997; 97US-0048351.
PR	30-MAY-1997; 97US-0048352.
PR	30-MAY-1997; 97US-0048355.
PR	05-AUG-1997; 97US-0054804.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;
PI	Greene JM, Hu JS, Lafleur DM, Moore PA, Ni J, Olsen HS;
PI	Rosen CA, Ruben SM, Shi Y, Young P;
XX	
DR	WPI; 1999-070066/06.
DR	P-PSDB; AAW67852.
XX	
PT	New isolated human genes and the secreted polypeptides they encode -
PT	useful for diagnosis and treatment of e.g. cancers, neurological
PT	disorders, immune diseases, inflammation or blood disorders
XX	
PS	Claim 1; Page 209-210; 385pp; English.
XX	
CC	This sequence represents a nucleic acid molecule which encodes a
CC	secreted human protein. The gene number, and the clone it is derived
CC	from, are detailed in the descriptor line. The gene can be used to
CC	generate fusion proteins by linking to the gene to a human immunoglobulin
CC	Fc portion (e.g. AAX00602) for increasing the stability of the new
CC	protein as compared to the human protein only.
CC	The invention relates to 87 novel genes and their fragments (nucleic
CC	acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)
CC	which are useful for preventing, treating or ameliorating medical
CC	conditions e.g. by protein or gene therapy. Also, pathological
CC	conditions can be diagnosed by determining the amount of the new
CC	polypeptides in a sample or by determining the presence of mutations in
CC	the new polynucleotides. Specific uses are described for each of the 87
CC	polynucleotides, based on which tissues they are most highly expressed in
CC	(see AAX00611 for described uses).
XX	
XQ	Sequence 1507 BP; 350 A; 456 C; 479 G; 213 T; 9 other;

Db 813 GATCTGAACAGGATGGGCACCTGGATGGAGGTG 851

RESULT 15

AA41603
ID AAL41603 standard; cDNA; 1507 BP.

XX AAL41603;

DT 19-APR-2002 (first entry)

XX Human colon cancer related coding sequence SEQ ID NO: 15.

XX Human: colon cancer; cytostatic; drug design; adenomatous polyp;
KW colorectal carcinoma; high metastatic potential colon tumour;
KW metastatic colon cancer; gene; ss.

OS Homo sapiens.

XX WO200196523-A2.

XX 20-DEC-2001.

PF 15-JUN-2001; 2001WO-US19313.

PR 15-JUN-2000; 2000US-211835P.

PA (CHIR) CHIRON CORP.

XX Kennedy GC, Kang S, Reinhard C, Jefferson AB;

XX WPI; 2002-164362/21.

XX Detecting a cancerous colon cell, useful for diagnosing colon cancer
PT and for rational drug and therapy design, comprises detecting at least
PT one differentially expressed gene product

PS Claim 42; Page 107; 135pp; English.

XX The present invention relates to methods for detecting a cancerous colon
CC cell involving detecting at least one differentially expressed gene such
CC as those given in AAL41595-AAL41611. This is useful for diagnosing colon
CC cancer, in rational drug and therapy design, and for identifying
CC additional genes linked to the development or inhibition of development
CC of colon cancer. Examples of colon cancer which can be detected include
CC adenomatous polyp, colorectal carcinoma, high metastatic potential colon
CC tumours and metastatic colon cancer. The present sequence is a colon
CC cancer associated protein coding sequence.

XX SQ Sequence 1507 BP; 350 A; 456 C; 479 G; 213 T; 9 other;

Alignment Scores:

Pred. No.:	0.00192	Length:	1507
Score:	70.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-768-840-1_COPY_254_266 (1-13) x AAL41603 (1-1507)

QY 1 AspLeuAsnIysAspGlyHisLeuAspGlySerGluVal 13

Db 813 GATCTGAACAGGATGGGCACCTGGATGGAGGTG 851

Search completed: May 19, 2003, 13:58:04
Job time.: 237 secs

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GenCore version 5.1.4.p5.4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 22:09:51 ; Search time 1746 seconds
(without alignments)
120.585 Million cell updates/sec

Title: US-09-768-840-1_copy_254_266
Perfect score: 70
Sequence: 1 DLNKGHLDGSEV 13

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09768840 @cgn_1_1_1906 -runat_14052003_095712_16653 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST : *
1: em_estba : *
2: em_esthum : *
3: em_estlin : *
4: em_estmu : *
5: em_estov : *
6: em_estpl : *
7: em_estro : *
8: em_hic : *
9: gb_est1 : *
10: gb_est2 : *
11: gb_est3 : *
12: gb_est4 : *
13: gb_est5 : *
14: gb_est6 : *
15: em_estfun : *
16: em_estom : *
17: gb_gss : *
18: em_gss_hum : *
19: em_gss_inv : *
20: em_gss_pin : *
21: em_gss_vrt : *
22: em_gss_fun : *
23: em_gss_mam : *
24: em_gss_mus : *
25: em_gss_other : *
26: em_gss_pro : *
27: em_gss_rod : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	515	9	AA456267
2	70	100.0	554	12	BG742111
3	70	100.0	588	9	AI751749
4	70	100.0	624	13	BM716710
5	70	100.0	824	13	BI820206
6	70	100.0	900	9	AL569912
7	70	100.0	909	9	AL520512
8	70	100.0	931	12	BE880649
9	70	100.0	954	9	AL573989
10	70	100.0	1092	9	AL544155
11	66	94.3	601	14	BM695756
12	64	91.4	324	14	H74164
13	64	91.4	664	14	BQ374092
14	64	91.4	1005	9	AA520513
15	62	88.6	341	9	AA239568
16	62	88.6	401	14	W64383
17	62	88.6	532	12	BG347022
18	62	88.6	578	14	BQ564168
19	62	88.6	582	12	BF118990
20	62	88.6	583	10	AW550048
21	62	88.6	618	10	AW558437
22	62	88.6	676	10	BB398523
23	62	88.6	678	10	BB041431
24	62	88.6	693	14	BQ209584
25	62	88.6	694	14	BQ192961
26	62	88.6	696	14	BM934252
27	62	88.6	867	13	BI903868
28	62	88.6	1009	9	AL570372
29	62	88.6	1112	11	AK003918
30	61	87.1	395	10	BE015071
31	61	87.1	465	10	AW353288
32	61	87.1	478	10	AW653432
33	61	87.1	481	9	AI341112
34	61	87.1	574	13	BI344949
35	61	87.1	596	13	BI337575
36	61	87.1	852	9	AL543274
37	60	85.7	660	14	BQ182243
38	60	85.7	660	14	BQ773463
39	58	82.9	362	14	W54172
40	57	81.4	662	10	AW578296
41	57	81.4	1070	14	BM903507
42	54	77.1	658	14	BQ044993
43	53	75.7	558	14	BM900368
44	53	75.7	629	13	BM138832
45	52	74.3	438	12	BF988162

ALIGNMENTS

RESULT 1
AA456267
LOCUS
DEFINITION
AA456267
515 bp mRNA linear EST 06-JUN-1997
zx99f04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811903 5', similar to SW:RCAL_MOUSE Q05186 RETICULOCALBIN PRECURSOR. ; mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 515)
Hillier L., Allen M., Bowles L., Dubuque T., Gelsel G., Jost S.,

Tue May 20 14:43:31 2003

Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0634 row: b column: 21
High quality sequence start: 3
High quality sequence stop: 554.
High quality sequence stop: 554.

TITLE
JOURNAL
COMMENT

Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

High quality sequence stop: 464.

Location/Qualifiers
1. 515
/organism="Homo sapiens"
/db_xref="GDB:6042814"
/db_xref="taxon:9606"
/clone="IMAGE:811903"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NbHPU, and fetal heart NbH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

FEATURES
source

BASE COUNT 115 a 142 c 180 g 78 t
ORIGIN
Alignment Scores:
Pred. No.: 0.018 Length: 515
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-768-840-1_COPY_254_266 (1-13) x AA456267 (1-515)
QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
DB 259 GATCTGAACAAGGATGGGACCTGGATGGAGTGAGGTG 297
RESULT 2
BG742111 554 bp mRNA linear EST 15-MAY-2001
LOCUS 602633581F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4778420 5', mRNA sequence.
DEFINITION
ACCESSION BG742111 GI:14052764
VERSION BG742111
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 554)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

FEATURES
source

BASE COUNT 131 a 146 c 194 g 83 t
ORIGIN
Alignment Scores:
Pred. No.: 0.02 Length: 554
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-09-768-840-1_COPY_254_266 (1-13) x BG742111 (1-554)
QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
DB 274 GATCTGAACAAGGATGGGACCTGGATGGAGTGAGGTG 312
RESULT 3
AI751749 588 bp mRNA linear EST 20-JUN-2002
LOCUS AI751749
DEFINITION clone NHTBC_cnl1f1 random, mRNA sequence.
ACCESSION AI751749
VERSION AI751749.1 GI:5130013
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 588)
Jia, L.B., Young, M.F., Touchman, J.W., Bouffard, G.G., Beckstrom-Sternberg, S.M., Green, E.D., Powell, J.I., Yang, L.M., Robey, P.G., Hotchkiss, R.N. and Francomano, C.A.
SGAP: The Skeletal Genome Anatomy Project
Unpublished (1997)
Contact: Libin Jia
Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 11 row: f column: 11
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
1. 588
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NHTBC_cnl1f1"
/clone_lib="Normal Human Trabecular Bone Cells"
/sex="Female"
/tissue_type="Bone"
/cell_type="Trabecular Bone Cells"


```

/lab_host="SURE"
/notes="Organ: Hip; Vector: pbluescript; Site_1: EcoRI;
Library constructed by Dr. Marian Young and Dr. Pamela
Gehron Robey (NIDCR)." 98 t 3 others

BASE COUNT 127 a 165 c 195 g 98 t 3 others
ORIGIN

Alignment Scores:
Pred. No.: 0.0218 Length: 588
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AT751749 (1-588)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 167 GATCTGAACAAGGATGGGACCTGGATGGAGTGAGGTG 205

RESULT 4
BM716710
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 624)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.

FEATURES
Location/Qualifiers
1..624
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-ahg-p-08-0-UI"
/clone_lib="UI-E-EJ0"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/notes="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoRI; Site_2: Not I;
UI-E-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoRI adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of

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first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA
; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT;
optic nerve, CCATTAAAGTG; retina, CCGCG; Retina Foveal and
Macular, GTCC; RPE and Choroid, ACCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI).

BASE COUNT 142 a 174 c 215 g 93 t
ORIGIN

Alignment Scores:
Pred. No.: 0.0237 Length: 624
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x BM716710 (1-624)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 349 GATCTGAACAAGGATGGGACCTGGGACGAGTGAGGTG 387

RESULT 5
BI820206
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 824)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11443 row: p column: 09
High quality sequence stop: 801.

FEATURES
Location/Qualifiers
1..824
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5178104"
/clone_lib="NIH-MGC_115"
/lab_host="DH10B"
/notes="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH-MGC Library."

BASE COUNT 180 a 227 c 298 g 119 t
ORIGIN

Alignment Scores:

```


pred. No.: 0.0354 Length: 824
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x B1820206 (1-824),

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
 |||||||||||||||||||||||||||||||||||||||
 DB 638 GATCTGAACAAGGATGGCCACCTGGATGGAGTGAGTG 676

RESULT 6

AL569912/c AL569912 900 bp mRNA linear EST 16-FEB-2001
 LOCUS AL569912 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI001YH07 3
 DEFINITION prime, mRNA sequence.

ACCESSION AL569912

VERSION AL569912.1 GI:12925723

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 900)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1..900

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CSODI001YH07"

/clone_lib="LTI_NFL006_PL2"

/tissue_type="placenta"

/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 143 a 270 c 285 g 195 t 7 others

ORIGIN

Alignment Scores:
 Pred. No.: 0.0401 Length: 900
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AL569912 (1-900)

Qy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

|||||||||||||||||||||||||||||||||||||

DB 582 GATCTGAACAAGGATGGCCACCTGGATGGAGTGAGTG 544

RESULT 7

AL520512/c AL520512 909 bp mRNA linear EST 13-FEB-2001
 LOCUS AL520512 LTI_NFL004_NBC2 Homo sapiens cDNA clone CSODB006YC08 3
 DEFINITION prime, mRNA sequence.

ACCESSION AL520512

VERSION AL520512.1 GI:12784005

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 909)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1..909

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CSODB006YC08"

/clone_lib="LTI_NFL004_NBC2"

/sex="male"

/tissue_type="neuroblastoma cells"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 142 a 278 c 291 g 197 t 1 others

ORIGIN

Alignment Scores:
 Pred. No.: 0.0407 Length: 909
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AL520512 (1-909)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

|||||||||||||||||||||||||||||||||||||

DB 586 GATCTGAACAAGGATGGCCACCTGGATGGAGTGAGTG 548

RESULT 8

BE880649

LOCUS

DEFINITION

601491556F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893989 5',

mRNA sequence.

ACCESSION BE880649

VERSION BE880649.1 GI:10329425

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 931)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTF/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LIAW682 row: 0 column: 14
 High quality sequence stop: 683.

FEATURES

source

Location/Qualifiers

1..931
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3893989"
 /clone_lib="NIH_MGC_69"
 /tissue_type="large cell carcinoma, undifferentiated"
 /lab_host="PH10B (phage-resistant)"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.1 kb. Library constructed by Life
 Technologies."

BASE COUNT 218 a 272 c 292 g 149 t
 ORIGIN

Alignment Scores:

Pred. No.: 0.0421 Length: 931
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x BE880649 (1-931)

QY 1 AspleuAnLysAspGlyHisLeuAspGlySerGluVal 13
 |||||
 Db 212 GATCTGAACAAGGATGGCACCCTGGATGGAGTGAGGTG 250

RESULT 9

AL573989/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr.

Location/Qualifiers

1..954

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DI053YN17"

/clone_lib="LTI_NFL006_PL2"

/tissue_type="placenta"

/note="Vector: pCMVSPORT 6; Site: 1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact: Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax: (1) 301 610 8371

Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com"

BASE COUNT 150 a 293 c 304 g 204 t 3 others

ORIGIN

Alignment Scores:

Pred. No.: 0.0437 Length: 954
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AL573989 (1-954)

QY 1 AspleuAnLysAspGlyHisLeuAspGlySerGluVal 13
 |||||
 Db 595 GATCTGAACAAGGATGGCACCCTGGATGGAGTGAGGTG 557

RESULT 10

AL544155

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr.

Location/Qualifiers

1..1092

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DI020YC22"

/clone_lib="LTI_NFL006_PL2"

/tissue_type="placenta"

/note="Vector: pCMVSPORT 6; Site: 1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact: Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax: (1) 301 610 8371

Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com"

BASE COUNT 231 a 313 c 389 g 156 t 3 others

ORIGIN

Alignment Scores:

Pred. No.: 0.053 Length: 1092
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AL544155 (1-1092)

QY 1 AspleuAnLysAspGlyHisLeuAspGlySerGluVal 13
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 Db 796 GATCTGAACAAGGATGGCACCCTGGATGGAGTGAGGTG 834

RESULT 11

BM695756

LOCUS

DEFINITION

UI-E-CQ1-aew-p-23-0-UI-r1

UI-E-CQ1-aew-p-23-0-UI 5', mRNA sequence.

BASE COUNT 601 bp mRNA linear EST 28-FEB-2002

UI-H-E20-bay-e-18-0-UI 3', mRNA sequence.

ACCESSION BQ574092
 VERSION BQ574092.1 GI:21477409
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 664)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
 Orthopaedics
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 Seq primer: M13 FORWARD
 POLYA-Yes.

FEATURES

source

Location/Qualifiers
 1..664
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-H-E20-bay-e-18-0-UI"
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 /tissue_type="Chondrosarcoma Grade II"
 /dev_stage="Adult"
 /lab_host="PH108 (Life Technologies)"
 /note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
 with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
 NCI-CGAP_Ch1 is a cDNA library containing the following
 tissue(s): Chondrosarcoma Grade II. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pT73-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 TGATCAGCT.
 TAG_LIB=UI-H-E20
 TAG_TISSUE=grade-2-chondrosarcoma
 TAG_SEQ=ATCTAATATG"

BASE COUNT 103 a 183 c 226 g 152 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.292 Length: 664
 Score: 64.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 91.43% Indels: 0
 DB: 14 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x BQ574092 (1-664)

QY 2 LeuAnLysAspGlyHisLeuAspGlySerGluVal 13
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 Db 662 CTGACACAGGATGGGCACCTGGATGGAGTG 627

RESULT 14

AL520513

LOCUS AL520513 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB006YC08 5
 DEFINITION prime, mRNA sequence.
 EST 13-FEB-2001
 linear 1005 bp mRNA

ACCESSION AL520513

AL520513.1 GI:12784006
 EST.
 human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1005)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

Location/Qualifiers
 1..1005
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DB006YC08"
 /clone_lib="LTI_NFL004_NBC2"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="DH108"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed
 by Life Technologies. Contact : Feng Liang Life
 Technologies, a division of Invitrogen 9800 Medical Center
 Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
 9371 Email : fliang@lifetech.com.URL :
<http://fulllength.invitrogen.com>"

BASE COUNT 221 a 250 c 359 g 150 t
 ORIGIN

Alignment Scores:

Pred. No.: 0.53 Length: 1005
 Score: 64.00 Matches: 12
 Percent Similarity: 92.31% Conservative: 0
 Best Local Similarity: 92.31% Mismatches: 1
 Query Match: 91.43% Indels: 0
 DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AL520513 (1-1005)

QY 1 AspLeuAnLysAspGlyHisLeuAspGlySerGluVal 13
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 Db 784 GATCTGAACAGGATGGGCACCTGGATGGAGTG 822

RESULT 15

AA239568

LOCUS

DEFINITION

AA239568 341 bp mRNA linear EST 12-MAR-1997
 mv22b09.r1 GuayWoodford Beiler mouse kidney day 0 Mus musculus cDNA
 clone IMAGE:65769 5' similar to gb:D13003 Mus musculus
 reticulocalbin mRNA, complete cds (MOUSE);, mRNA sequence.

ACCESSION

AA239568

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 341)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Willie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:401617
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 260.
Location/Qualifiers
1. .341
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="GuayWoodford Beiler mouse kidney day 0"
/tissue_type="kidney"
/dev_stage="newborn (day 0)"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: kidney; Vector: pBluescript SK-; Site_1:
EcORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Average insert size: 1.0 Kb; Uni-ZAP XR Vector;
-5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Library provided
Lisa Guay-Woodford."

BASE COUNT 79 a 96 c 109 g 57 t
ORIGIN

Alignment Scores:
Pred. No.: 0.251 Length: 341
Score: 62.00 Matches: 12
Percent Similarity: 92.31% Conservative: 0
Best Local Similarity: 92.31% Mismatches: 1
Query Match: 88.57% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AA239568 (1-341)

Qy 1 AspleuAnLysAspGlyHisLeuAspGlySerGluVal 13
Db 64 GATCTGAACAAGGACGGCGCAGTGGATGGCAGTGAAGTC 102

Search completed: May 20, 2003, 07:32:14
Job time : 1764 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003. CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 22:09:51 ; Search time 55 Seconds
(without alignments)
72.487 Million cell updates/sec

Title: US-09-768-840-1_COPY_254_266
Perfect score: 70
Sequence: 1 DLNKGDLGSEV 13

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -QMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
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-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO_XLPXY -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THRAD=3 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents.NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	1055	2	US-08-828-242-2
2	70	100.0	1055	4	US-09-206-499-2
3	70	100.0	1463	2	US-08-910-927B-2
4	70	100.0	1463	4	US-09-270-270-2
5	70	100.0	1490	4	US-09-484-970B-53
6	43	61.4	480	4	US-09-404-879A-60
7	43	61.4	531	4	US-09-404-879A-5
8	43	61.4	1613	4	US-09-061-154-1
9	43	61.4	1613	4	US-09-061-154-3
10	43	61.4	2017	4	US-09-404-879A-72
11	40	57.1	955	4	US-09-399-913-11
12	40	57.1	955	4	US-09-298-731-11

c 13	40	57.1	1185	3	US-09-023-339-3	Sequence 3, Appl
c 14	40	57.1	1260	3	US-09-023-173-5	Sequence 5, Appl
c 15	40	57.1	1308	3	US-09-023-173-10	Sequence 10, Appl
c 16	40	57.1	1308	3	US-09-023-339-6	Sequence 6, Appl
c 17	40	57.1	1463	4	US-09-399-913-1	Sequence 1, Appl
c 18	40	57.1	1463	4	US-09-298-731-1	Sequence 1, Appl
c 19	40	57.1	1534	4	US-09-399-913-7	Sequence 7, Appl
c 20	40	57.1	1534	4	US-09-298-731-7	Sequence 7, Appl
c 21	40	57.1	1540	4	US-09-399-913-9	Sequence 9, Appl
c 22	40	57.1	1540	4	US-09-298-731-9	Sequence 9, Appl
c 23	40	57.1	1856	4	US-09-399-913-3	Sequence 3, Appl
c 24	40	57.1	1856	4	US-09-298-731-3	Sequence 3, Appl
c 25	40	57.1	1907	4	US-09-399-913-5	Sequence 5, Appl
c 26	40	57.1	1907	4	US-09-298-731-5	Sequence 5, Appl
c 27	40	57.1	11907	4	US-08-061-376-4	Sequence 4, Appl
c 28	40	57.1	14255	1	US-08-320-559-1	Sequence 1, Appl
c 29	40	57.1	14255	1	US-08-327-392-1	Sequence 1, Appl
c 30	40	57.1	14255	1	US-08-306-691B-55	Sequence 55, Appl
c 31	40	57.1	14255	3	US-08-545-860D-1	Sequence 1, Appl
c 32	40	57.1	14255	5	PCT-US94-04496-1	Sequence 1, Appl
c 33	39	55.7	527	4	US-09-370-838-281	Sequence 281, App
c 34	39	55.7	942	4	US-09-134-001C-1534	Sequence 1534, Ap
c 35	39	55.7	1320	2	US-08-461-775-8	Sequence 8, Appl
c 36	39	55.7	1320	3	US-09-031-606-8	Sequence 8, Appl
c 37	39	55.7	1496	3	US-09-048-889-9	Sequence 9, Appl
c 38	39	55.7	1620	2	US-08-461-775-10	Sequence 10, Appl
c 39	39	55.7	1620	3	US-09-031-606-10	Sequence 10, Appl
c 40	39	55.7	2062	1	US-08-073-383-5	Sequence 5, Appl
c 41	39	55.7	2062	3	US-08-328-239A-3	Sequence 3, Appl
c 42	39	55.7	2062	5	PCT-US94-06365-5	Sequence 5, Appl
c 43	39	55.7	2062	5	PCT-US95-13661-3	Sequence 3, Appl
c 44	39	55.7	2167	2	US-08-461-775-9	Sequence 9, Appl
c 45	39	55.7	2167	3	US-09-031-606-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-08-828-242-2
; Sequence 2, Application US/08828242
; Patent No. 5871970

GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Inocyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1055 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: CONTUT01
CLONE: 2509570
US-08-828-242-2

Alignment Scores:
Pred. No.: 0.000118 Length: 1055
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-08-828-242-2 (1-1055)

QY 1 AspleuasnllyspGlyHisLeuAspGlySerGluVal 13
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Db 793 GATCTGAACAAGGATGGCCACCTGGATGGAGTGAGGTG 831

RESULT 2
; Sequence 2, Application US/09206499
; Patent No. 6194385
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/206,499
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,242
; FILING DATE: 03/31/1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1055 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: CONTUT01
CLONE: 2509570
US-09-206-499-2

Alignment Scores:
Pred. No.: 0.000118 Length: 1055
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

Pred. No.: 0.000118 Length: 1055
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-206-499-2 (1-1055)

QY 1 AspleuasnllyspGlyHisLeuAspGlySerGluVal 13
|||||
Db 793 GATCTGAACAAGGATGGCCACCTGGATGGAGTGAGGTG 831

RESULT 3
; Sequence 2, Application US/08910927B
; Patent No. 5976801
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,927B
; FILING DATE: Hereewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1463 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: RAYNOT02
CLONE: 922578
US-08-910-927B-2

Alignment Scores:
Pred. No.: 0.000173 Length: 1463
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-08-910-927B-2 (1-1463)

-Tue May 20 14:43:30 2003

us-09-768-840-1_copy_254_266.p2n.rni

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Qy 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 808 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGTG 846

RESULT 4
US-09-270-270-2
; Sequence 2, Application US/09270270
; Patent No. 6235477
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,270
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,927
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1463 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: RATROT02
; CLONE: 922578
US-09-270-270-2

Alignment Scores:
Pred. No.: 0.000173 Length: 1463
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 4

US-09-768-840-1_COPY_254_266 (1-13) x US-09-270-270-2 (1-1463)
Qy 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 808 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGTG 846

RESULT 5
US-09-484-970B-53
; Sequence 53, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:

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```

; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 53
; LENGTH: 1490
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 016193.3
; NAME/KEY: unsure
; LOCATION: 25
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-53

Alignment Scores:
Pred. No.: 0.000177 Length: 1490
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 4

US-09-768-840-1_COPY_254_266 (1-13) x US-09-484-970B-53 (1-1490)
Qy 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 841 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGTG 879

RESULT 6
US-09-404-879A-60
; Sequence 60, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-404-879A-60

Alignment Scores:
Pred. No.: 7.3 Length: 480
Score: 43.00 Matches: 8
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 3
Query Match: 61.43% Indels: 0
Gaps: 0
DB: 4

US-09-768-840-1_COPY_254_266 (1-13) x US-09-404-879A-60 (1-480)
Qy 1 AspleuAsnLysAspGlyHisLeuAspGlySerGlu 12
Db 209 GATCTGAACAGGATGGGAAGATGGACCAAGAG 244

RESULT 7
US-09-404-879A-5
; Sequence 5, Application US/09404879A

```



```
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462G2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 531
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-404-879A-5

Alignment Scores:
Pred. No.: 8.22 Length: 531
Score: 43.00 Matches: 8
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 3
Query Match: 61.43% Indels: 0
DB: 4 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-404-879A-5 (1-531)
QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGlu 12
| | | | | | | | | | | | | | | | | | | |
Db 237 GATCTGAACGAAGGATGGGAAGATGGACCAAGAG 272

RESULT 8
US-09-061-154-1/c
; Sequence 1, Application US/09061154
; Patent No. 6462188
; GENERAL INFORMATION:
; APPLICANT: Kirkness, E.
; TITLE OF INVENTION: NEW HUMAN 5-HT3 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,154
; FILING DATE: 16-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24366-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1613 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 67...1389
; OTHER INFORMATION:
US-09-061-154-3

Alignment Scores:
Pred. No.: 30.4 Length: 1613
Score: 43.00 Matches: 7
Percent Similarity: 81.82% Conservative: 2
Best Local Similarity: 63.64% Mismatches: 2
Query Match: 61.43% Indels: 0
DB: 4 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-061-154-1 (1-1613)
QY 3 AsnLysAspGlyHisLeuAspGlySerGluVal 13
| | | | | | | | | | | | | | | | | | | |
Db 1008 AACCAAGAAAGCCATGCGAGATGGTGAAGAAGTG 976

RESULT 9
US-09-061-154-3/c
; Sequence 3, Application US/09061154
; Patent No. 6462188
; GENERAL INFORMATION:
; APPLICANT: Kirkness, E.
; TITLE OF INVENTION: NEW HUMAN 5-HT3 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,154
; FILING DATE: 16-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24366-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1613 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 67...1389
; OTHER INFORMATION:
US-09-061-154-3

Alignment Scores:
Pred. No.: 30.4 Length: 1613
Score: 43.00 Matches: 7
Percent Similarity: 81.82% Conservative: 2
Best Local Similarity: 63.64% Mismatches: 2
Query Match: 61.43% Indels: 0
DB: 4 Gaps: 0
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DB: 4 Gaps: 0
US-09-768-840-1_COPY_254_266 (1-13) x US-09-061-154-3 (1-1613)
QY 3 AsnLysAspGlyHisLeuAspGlySerGluVal 13
  |||:||||| ||||| |||||
DB 1008 AACCAAGAGCGCATGCAGATGCTGAAGAAGTG 976

RESULT 10
US-09-404-879A-72
; Sequence 72, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 2017
; TYPE: DNA
; ORGANISM: Homo sapient
US-09-404-879A-72

Alignment Scores:
Pred. No.: 39.6 Length: 2017
Score: 43.00 Matches: 8
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 3
Query Match: 61.43% Indels: 0
DB: 4 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-404-879A-72 (1-2017)
QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGlu 12
  |||:||||| ||||| |||||
DB 237 GATCTGAACAGGATGGGAAGATGGACCAAGAG 272

RESULT 11
US-09-399-913-11
; Sequence 11, Application US/09399913
; Patent No. 6361971
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: Betty, Maria
; APPLICANT: Ling, Hwai-Ping
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
; FILE REFERENCE: MNI-070CP2
; CURRENT APPLICATION NUMBER: US/09/399,913
; CURRENT FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: USSN 09/350,614
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 09/350,874
; EARLIER FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 955
; TYPE: DNA

; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (345)..(953)
; FEATURE:
; OTHER INFORMATION: Xaa at position 92 of the corresponding amino acid
; OTHER INFORMATION: sequence may be any amino acid
US-09-399-913-11

Alignment Scores:
Pred. No.: 62 Length: 955
Score: 40.00 Matches: 6
Percent Similarity: 84.62% Conservative: 5
Best Local Similarity: 46.15% Mismatches: 2
Query Match: 57.14% Indels: 0
DB: 4 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-298-731-11 (1-955)
QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
  |||:||||| ||||| |||||
DB 795 GACATCAATAAAGCGGCTACATAAACAAGAGGAGATG 833

RESULT 12
US-09-298-731-11
; Sequence 11, Application US/09298731
; Patent No. 6369197
; GENERAL INFORMATION:
; APPLICANT: KENNETH RHODES, MARIA BETTY, HUIAI-PING LING, AND FRANK AN
; TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
; FILE REFERENCE: MNI-070
; CURRENT APPLICATION NUMBER: US/09/298,731
; CURRENT FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (345)..(953)
; FEATURE:
; OTHER INFORMATION: Xaa at position 92 of the corresponding amino acid
; OTHER INFORMATION: sequence may be any amino acid
US-09-298-731-11

Alignment Scores:
Pred. No.: 62 Length: 955
Score: 40.00 Matches: 6
Percent Similarity: 84.62% Conservative: 5
Best Local Similarity: 46.15% Mismatches: 2
Query Match: 57.14% Indels: 0
DB: 4 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-298-731-11 (1-955)
QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
  |||:||||| ||||| |||||
DB 795 GACATCAATAAAGCGGCTACATAAACAAGAGGAGATG 833

RESULT 13
US-09-023-339-3/C
; Sequence 3, Application US/09023339
; Patent No. 6127145
; GENERAL INFORMATION:
; APPLICANT: Sutliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of '1-Antitrypsin
; TITLE OF INVENTION: in plants
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
```



```
;; STREET: P.O. Box 60850
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94306
;; COMPUTER READABLE FORM:
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/023,339
;; FILING DATE: 13-FEB-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/037,991
;; FILING DATE: 13-FEB-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Petithory, Joanne R
;; REGISTRATION NUMBER: P42,995
;; REFERENCE/DOCKET NUMBER: 0665-0003.30
;; TELEPHONE: 650-324-0880
;; TELEFAX: 650-324-0960
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1185 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; CLONE: codon-optimized AAT coding sequence
US-09-023-339-3

Alignment Scores:
Pred. No.: 79.9 Length: 1185
Score: 40.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 57.14% Indels: 0
DB: 3 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-023-339-3 (1-1185)
QY 1 AspleuAsnLysAspGlyHisLeuAspGly 10
||||| :|||||
Db 1092 GACCTCGGCGGATGGACATGGGATGGC 1063

RESULT 14
US-09-023-173-5/c
; Sequence 5, Application US/09023173
; Patent No. 6066781
; GENERAL INFORMATION:
; APPLICANT: Sutliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of Mature Proteins
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,173
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 435
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/038,168
;; FILING DATE: 13-FEB-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Petithory, Joanne R
;; REGISTRATION NUMBER: P42995
;; REFERENCE/DOCKET NUMBER: 0665-0007.30
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-324-0880
;; TELEFAX: 650-324-0960
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1260 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; CLONE: codon-optimized Ramy3D signal-mature AAT
US-09-023-173-5

Alignment Scores:
Pred. No.: 85.9 Length: 1260
Score: 40.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 57.14% Indels: 0
DB: 3 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-023-173-5 (1-1260)
QY 1 AspleuAsnLysAspGlyHisLeuAspGly 10
||||| :|||||
Db 1167 GACCTCGGCGGATGGACATGGGATGGC 1138

RESULT 15
US-09-023-173-10/c
; Sequence 10, Application US/09023173
; Patent No. 6066781
; GENERAL INFORMATION:
; APPLICANT: Sutliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of Mature Proteins
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,173
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,168
; FILING DATE: 13-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R
; REGISTRATION NUMBER: P42995
; REFERENCE/DOCKET NUMBER: 0665-0007.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1308 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-023-173-10

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Alignment Scores:
Pred. No.:      89.8      Length:      1308
Score:          40.00     Matches:       7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches:  2
Query Match:      57.14% Indels:       0
DB:               3      Gaps:        0

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US-09-768-840-1_COPY_254_266 (1-13) x US-09-023-173-10 (1-1308)

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Qy  1 AspLeuAsnLysAspGlyHisLeuAspGly 10
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Db 1208 GACCTCGGGCGGGATGGACATGGGATGGC 1179

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Job time : 68 secs

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GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 22:09:52 ; Search time 714 Seconds
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Title: US-09-768-840-1_COPY_254_266
Perfect score: 70
Sequence: 1 DLNKGHLGDSV 13

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-MAXLEN=2000000000 -USER=US09768840 -CCGN_1_1_130 -runat_14052003_095714_16679
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	70	100.0	1463	10	US-09-847-809A-2
3	70	100.0	1503	9	US-09-905-291A-220
4	70	100.0	1503	9	US-09-902-853-220

5	70	100.0	1503	9	US-09-907-824-220	Sequence 220, App
6	70	100.0	1503	9	US-09-907-841-220	Sequence 220, App
7	70	100.0	1503	9	US-09-904-011-220	Sequence 220, App
8	70	100.0	1503	9	US-10-028-072-363	Sequence 363, App
9	70	100.0	1503	9	US-09-906-743-220	Sequence 220, App
10	70	100.0	1503	9	US-10-121-049-363	Sequence 363, App
11	70	100.0	1503	9	US-10-123-904-363	Sequence 363, App
12	70	100.0	1503	9	US-10-140-470-363	Sequence 363, App
13	70	100.0	1503	9	US-09-906-838-220	Sequence 220, App
14	70	100.0	1503	9	US-09-907-613-220	Sequence 220, App
15	70	100.0	1503	9	US-09-907-943-220	Sequence 220, App
16	70	100.0	1503	9	US-10-175-748-363	Sequence 363, App
17	70	100.0	1503	9	US-10-176-918-363	Sequence 363, App
18	70	100.0	1503	9	US-10-176-921-363	Sequence 363, App
19	70	100.0	1503	9	US-10-137-865-363	Sequence 363, App
20	70	100.0	1503	9	US-10-140-474-363	Sequence 363, App
21	70	100.0	1503	9	US-09-904-820-220	Sequence 220, App
22	70	100.0	1503	9	US-09-904-859-220	Sequence 220, App
23	70	100.0	1503	9	US-09-909-204-220	Sequence 220, App
24	70	100.0	1503	9	US-10-142-431-363	Sequence 363, App
25	70	100.0	1503	9	US-10-143-114-363	Sequence 363, App
26	70	100.0	1503	9	US-09-904-786-220	Sequence 220, App
27	70	100.0	1503	9	US-09-906-646-220	Sequence 220, App
28	70	100.0	1503	9	US-09-906-700-220	Sequence 220, App
29	70	100.0	1503	9	US-10-140-002-363	Sequence 363, App
30	70	100.0	1503	9	US-09-902-903-220	Sequence 220, App
31	70	100.0	1503	9	US-09-903-749A-220	Sequence 220, App
32	70	100.0	1503	9	US-09-903-786-220	Sequence 220, App
33	70	100.0	1503	9	US-10-142-419-363	Sequence 363, App
34	70	100.0	1503	9	US-09-902-736-220	Sequence 220, App
35	70	100.0	1503	9	US-09-904-119-220	Sequence 220, App
36	70	100.0	1503	9	US-09-904-956-220	Sequence 220, App
37	70	100.0	1503	9	US-09-907-794-220	Sequence 220, App
38	70	100.0	1503	9	US-10-123-262-363	Sequence 363, App
39	70	100.0	1503	9	US-10-142-423-363	Sequence 363, App
40	70	100.0	1503	9	US-09-903-692-220	Sequence 220, App
41	70	100.0	1503	9	US-09-903-520-220	Sequence 220, App
42	70	100.0	1503	9	US-09-903-943-220	Sequence 220, App
43	70	100.0	1503	9	US-09-904-462-220	Sequence 220, App
44	70	100.0	1503	9	US-09-905-056-220	Sequence 220, App
45	70	100.0	1503	9	US-09-907-925-220	Sequence 220, App

ALIGNMENTS

RESULT 1
US-09-768-840-2
; Sequence 2, Application US/09768840
; Patent No. US20010012831A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; APPLICATION NUMBER: US/09/768,840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/206,499


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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1055 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COMUT01
; CLONE: 2509570
; US-09-768-840-2
;
; Alignment Scores:
; Pred. No.: 0.000101 Length: 1055
; Score: 70.00 Matches: 13
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 100.00% Indels: 0
; DB: 10 Gaps: 0
;
; US-09-768-840-1_COPY_254_266 (1-13) x US-09-768-840-2 (1-1055)
;
; QY 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13
; DB 793 GATCTGAACAAGGATGGCCACCTGGATGGAGTGAGGTG 831
;
; RESULT 2
; US-09-847-809A-2
; Sequence 2, Application US/09847809A
; Patent No. US20020081604A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Lal, Preeti
; Corley, Neil C.
; Shah, Purvi
;
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 01-May-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/270,270
; FILING DATE: 1999-03-16
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1463 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: RATRNOT02
; CLONE: 922578
; US-09-847-809A-2
;
; Alignment Scores:
; Pred. No.: 0.000147 Length: 1463
; Score: 70.00 Matches: 13
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 100.00% Indels: 0
; DB: 10 Gaps: 0
;
; US-09-768-840-1_COPY_254_266 (1-13) x US-09-847-809A-2 (1-1463)
;
; QY 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13
; DB 808 GATCTGAACAAGGATGGCCACCTGGATGGAGTGAGGTG 846
;
; RESULT 3
; US-09-905-291A-220
; Sequence 220, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 220
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-291A-220

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Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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US-09-768-840-1_copy_254_266 (1-13) x US-09-905-291A-220 (1-1503)

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Oy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
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Db 794 GATCTGACACAGGATGGGCACCTGGATGGAGTGAGGTG 832

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RESULT 4

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US-09-902-853-220
; Sequence 220, Application US/0902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:

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; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.

```

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 220
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-902-853-220

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Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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US-09-768-840-1_copy_254_266 (1-13) x US-09-902-853-220 (1-1503)

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Oy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 794 GATCTGACACAGGATGGGCACCTGGATGGAGTGAGGTG 832

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RESULT 5

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US-09-907-824-220
; Sequence 220, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:

```

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; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

```


APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 220
LENGTH: 1503
TYPE: DNA
ORGANISM: Homo Sapien
US-09-907-824-220

Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-907-824-220 (1-1503)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 794 GATCTCAACAAGGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 6
US-09-907-841-220
; Sequence 220, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 220
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-841-220

Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-907-841-220 (1-1503)

Qy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 794 GATCTGAACAAGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 7

US-09-904-011-220

; Sequence 220, Application US/09904011

; Publication No. US20030003530A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/904,011

; CURRENT FILING DATE: 2001-07-11

; PRIOR APPLICATION NUMBER: 09/665,350

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219

; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 220

; LENGTH: 1503

; TYPE: DNA

; ORGANISM: Homo Sapien

US-09-904-011-220

Alignment Scores:

Pred. No.: 0.000151 Length: 1503

Score: 70.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-904-011-220 (1-1503)

Qy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 794 GATCTGAACAAGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 8

US-10-028-072-363

; Sequence 363, Application US/10028072

; Publication No. US20030004311A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang

; TITLE OF INVENTION:

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/028,072

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588

PRIOR APPLICATION NUMBER: 60/079294	PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663	PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728	PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165	PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203	PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229	PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695	PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/081817	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999	PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086414	PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086430	PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087106	PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/088026	PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088730	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088741	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858	PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089532	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907	PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947	PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090349	PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445	


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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

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Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

```

```

US-09-768-840-1_COPY_254_266 (1-13) x US-10-028-072-363 (1-1503)

```

```

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

```

```

Db 794 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 832

```

```

RESULT 9

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US-09-906-742-220

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; Sequence 220, Application US/09906742

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```

; Publication No. US20030023054A1

```

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; GENERAL INFORMATION:

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; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paonl, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-07-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08

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; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 220
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-742-220

```

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Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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```

US-09-768-840-1_COPY_254_266 (1-13) x US-09-906-742-220 (1-1503)

```

```

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

```

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Db 794 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 832

```

```

RESULT 10

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US-10-121-049-363

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; Sequence 363, Application US/10121049

```

```

; Publication No. US2003002239A1

```

```

; GENERAL INFORMATION:

```

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

```

```

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm

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; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 363
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-121-049-363

Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-10-121-049-363 (1-1503)

Qy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 794 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 11
US-10-123-904-363
; Sequence 363, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 363
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-904-363

Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-10-123-904-363 (1-1503)

Qy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 794 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 12
US-10-140-470-363
; Sequence 363, Application US/10140470
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; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 363
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-470-363

Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-10-140-470-363 (1-1503)

Qy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 794 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 13
US-09-906-838-220
; Sequence 220, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
```



```

; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 220
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-838-220

Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-906-838-220 (1-1503)
Qy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 794 GATCTGAACAGGATGGACCTGGATGGAGTGAGTG 832

RESULT 14
US-09-907-613-220
; Sequence 220, Application US/09907613
; GENERAL INFORMATION:
; Publication No. US20030027145A1
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David

```

```

; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 220
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-613-220

Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

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Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	70	100	0	327	9	US-09-984-245-166	Sequence 166, App
2	70	100	0	327	9	US-09-966-262-166	Sequence 166, App
3	70	100	0	327	9	US-09-983-963-166	Sequence 166, App
4	70	100	0	327	9	US-10-143-090-166	Sequence 166, App
5	70	100	0	328	9	US-09-905-291A-221	Sequence 221, App
6	70	100	0	328	9	US-09-903-853-221	Sequence 221, App
7	70	100	0	328	9	US-09-907-824-221	Sequence 221, App
8	70	100	0	328	9	US-09-907-841-221	Sequence 221, App
9	70	100	0	328	9	US-09-904-011-221	Sequence 221, App
10	70	100	0	328	9	US-10-028-072-364	Sequence 364, App
11	70	100	0	328	9	US-09-906-742-221	Sequence 221, App
12	70	100	0	328	9	US-10-121-049-364	Sequence 364, App
13	70	100	0	328	9	US-10-123-904-364	Sequence 364, App
14	70	100	0	328	9	US-10-140-470-364	Sequence 364, App
15	70	100	0	328	9	US-09-906-838-221	Sequence 221, App
16	70	100	0	328	9	US-09-907-613-221	Sequence 221, App
17	70	100	0	328	9	US-09-907-942-221	Sequence 221, App
18	70	100	0	328	9	US-10-175-748-364	Sequence 364, App
19	70	100	0	328	9	US-10-176-916-364	Sequence 364, App

Tue May 20 14:43:32 2003

us-09-768-840-1_copy_254_266.rapb

; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 166
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (300)
; OTHER INFORMATION: Xaa equals any of the L-amino acids commonly found in naturally
; OTHER INFORMATION: proteins
US-09-984-245-166

Query Match 100.0%; Score 70; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSEV 13
Db 253 DLNKGHLDGSEV 265

RESULT 2
US-09-966-262-166
; Sequence 166, Application US/09966262
; Publication No. US20030050461A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/966,262
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937

; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 166
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (300)
; OTHER INFORMATION: Xaa equals any of the L-amino acids commonly found in naturally
; OTHER INFORMATION: proteins
US-09-966-262-166

Query Match 100.0%; Score 70; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSEV 13
Db 253 DLNKGHLDGSEV 265

RESULT 3
US-09-983-966-166
; Sequence 166, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/983,966
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21

;; PRIOR APPLICATION NUMBER: US 60/041,281
;; PRIOR FILING DATE: 1997-03-21
;; PRIOR APPLICATION NUMBER: US 60/048,094
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,350
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,188
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,135
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/050,937
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,187
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,099
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,352
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,186
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,069
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,095
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,131
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,096
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,355
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,160
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,351
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,154
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/054,804
;; PRIOR FILING DATE: 1997-08-05
;; PRIOR APPLICATION NUMBER: US 60/056,370
;; PRIOR FILING DATE: 1997-08-19
;; PRIOR APPLICATION NUMBER: US 60/060,862
;; PRIOR FILING DATE: 1997-10-02
;; NUMBER OF SEQ ID NOS: 343
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 166
;; LENGTH: 327
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: MISC_FEATURE
;; LOCATION: (300)
;; OTHER INFORMATION: Xaa equals any of the L-amino acids commonly found in naturally
US-09-983-966-166

Query Match 100.0%; Score 70; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DLNKGDLGSEV 13
DB 253 DLNKGDLGSEV 265
|||||

RESULT 4
US-10-143-090-166
;; Sequence 166, Application US/10143090
;; Publication No. US20030069406A1
;; GENERAL INFORMATION:
;; APPLICANT: Young et al.
;; TITLE OF INVENTION: 87 Human Secreted Proteins
;; FILE REFERENCE: P2004P1
;; CURRENT APPLICATION NUMBER: US/10/143,090

;; CURRENT FILING DATE: 2002-05-13
;; PRIOR APPLICATION NUMBER: 09/154,707
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 343
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 166
;; LENGTH: 327
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: MISC_FEATURE
;; LOCATION: (300)
;; OTHER INFORMATION: Xaa equals any of the L-amino acids commonly found in naturally
US-10-143-090-166

Query Match 100.0%; Score 70; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DLNKGDLGSEV 13
DB 253 DLNKGDLGSEV 265
|||||

RESULT 5

US-09-905-291A-221
;; Sequence 221, Application US/09905291A
;; Patent No. US20020160374A1
;; GENERAL INFORMATION:

;; APPLICANT: Genentech, Inc.
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, A.
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth, J.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Mather, Jennie P.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/905,291A
;; CURRENT FILING DATE: 2001-07-12
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15


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; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-291A-221

Query Match      100.0%; Score 70; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 DLNKGHLDGSEV 13
Db  254 DLNKGHLDGSEV 266

RESULT 6
US-09-902-853-221
; Sequence 221, Application US/09502853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-853-221

Query Match      100.0%; Score 70; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 DLNKGHLDGSEV 13
Db  254 DLNKGHLDGSEV 266

RESULT 7
US-09-907-824-221
; Sequence 221, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
PRIOR FILING DATE: 2001-07-17
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-824-221

Query Match 100.0%; Score 70; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
DB 254 DLNKGHLDGSEV 266

RESULT 8

US-09-907-841-221
Sequence 221, Application US/09907841
Publication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-841-221

Query Match 100.0%; Score 70; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
DB 254 DLNKGHLDGSEV 266

RESULT 9

US-09-904-011-221
Sequence 221, Application US/09904011
Publication No. US20030003530A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen


```

; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-221

Query Match 100.0%; Score 70; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSEV 13
Db 254 DLNKGHLDGSEV 266
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```

RESULT 10
US-10-028-072-364
; Sequence 364, Application US/10028072
; Publication NO. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filwaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059836
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062814
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/063127
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063327
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063550
; PRIOR FILING DATE: 1997-10-28
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;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063704
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;; PRIOR FILING DATE: 1997-10-29
;; PRIOR APPLICATION NUMBER: 60/063755
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/064248
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;; PRIOR APPLICATION NUMBER: 60/069334
;; PRIOR FILING DATE: 1997-12-11
;; PRIOR APPLICATION NUMBER: 60/069694
;; PRIOR FILING DATE: 1997-12-16
;; PRIOR APPLICATION NUMBER: 60/072320
;; PRIOR FILING DATE: 1998-01-23
;; PRIOR APPLICATION NUMBER: 60/073612
;; PRIOR FILING DATE: 1998-02-04
;; PRIOR APPLICATION NUMBER: 60/074086
;; PRIOR FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: 60/074092
;; PRIOR FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079663
;; PRIOR FILING DATE: 1998-02-27
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/080165
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/081203
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081229
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;; PRIOR FILING DATE: 1998-05-07

;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR FILING DATE: 1998-05-12
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;; PRIOR FILING DATE: 1998-05-28
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;; PRIOR APPLICATION NUMBER: 60/088810
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;; PRIOR APPLICATION NUMBER: 60/088858
;; PRIOR FILING DATE: 19/98-06-11
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090538
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07

Query Match Best Local Similarity 100.0%; Score 70; DB 9; Length 328;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
Db 254 DLNKGHLDGSEV 266
|||||||

RESULT 11
US-09-906-742-221
; Sequence 221, Application US/09906742
; Publication No. US2003023054A1
; GENERAL INFORMATION:

Query Match 100.0%; Score 70; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSEV 13
Db 254 DLNKGHLDGSEV 266

RESULT 12

US-10-121-049-364
; Sequence 364, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 364
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-364

Query Match 100.0%; Score 70; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSEV 13
Db 254 DLNKGHLDGSEV 266

RESULT 13

US-10-123-904-364
; Sequence 364, Application US/10123904
; Publication No. US20030022238A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-742-221


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; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC34
; CURRENT APPLICATION NUMBER: US/10/123,904
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 364
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-364

Query Match      100.0%  Score 70; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
Db 254 DLNKGHLDGSEV 266

RESULT 14
US-10-140-470-364
; Sequence 364, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC160
; CURRENT APPLICATION NUMBER: US/10/140,470
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 364
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-364

Query Match      100.0%  Score 70; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
Db 254 DLNKGHLDGSEV 266

RESULT 15
US-09-906-838-221
; Sequence 221, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
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; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
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; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
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; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-838-221
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us-09-768-840-1_copy_254_266.rapb

Tue May 20 14:43:32 2003

Query Match 100.0%; Score 70; DB 9; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00034;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLNKGHLGSEV 13
 | | | | | | | | | | | | | | |
 Db 254 DLNKGHLGSEV 266

Search completed: May 14, 2003, 10:47:54
 Job time : 1.25806 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2003, 10:40:07 ; Search time 4.1173 Seconds
(without alignments)
650.575 Million cell updates/sec

Title: us-09-768-840-1_copy_254_266

Perfect score: 70
Sequence: 1 DLNKGHLGSGEV 13

Scoring table:

BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	328	4 Q9HBZ8	Q9hbz8 homo sapien
2	70	100.0	328	4 Q96D15	Q96d15 homo sapien
3	62	88.6	259	11 Q9CTD4	Q9ctd4 mus musculus
4	62	88.6	315	11 Q9BK35	Q9bk35 mus musculus
5	62	88.6	328	11 Q8R137	Q8r137 mus musculus
6	48	68.6	384	4 Q96NQ4	Q96nq4 homo sapien
7	48	68.6	482	4 Q9BV35	Q9bv35 homo sapien
8	47	67.1	599	11 Q91WH8	Q91wh8 mus musculus
9	47	67.1	864	4 Q3UBC2	Q3ubc2 homo sapien
10	47	67.1	907	11 Q60902	Q60902 mus musculus
11	46	65.7	127	5 Q22159	Q22159 caenorhabdi
12	45	64.3	289	16 Q9PM44	Q9pm44 campylobact
13	44	62.9	322	13 Q93434	Q93434 fugu rubrip
14	44	62.9	343	5 Q9U460	Q9u460 plasmodium
15	44	62.9	592	2 Q9RDT6	Q9rdt6 rhodospiril
16	44	62.9	737	2 Q9EYQ5	Q9eyq5 clostridium

17	43	61.4	163	13	012996	O12996 xenopus lae
18	43	61.4	163	13	012997	O12997 xenopus lae
19	43	61.4	236	5	076670	O76670 caenorhabdi
20	43	61.4	666	10	Q8VZP8	Q8vzp8 arabidopsis
21	43	61.4	756	2	Q92NN6	Q92nn6 bacillus sp
22	43	61.4	1181	10	Q9X116	Q9x116 arabidopsis
23	42	60.0	142	10	064866	O64866 arabidopsis
24	42	60.0	186	5	Q20796	Q20796 caenorhabdi
25	42	60.0	189	13	Q90WX4	Q90wx4 brachydanio
26	42	60.0	189	13	Q8UWA4	O8uwa4 oryzias lat
27	42	60.0	189	13	Q8UUY1	O8uyy1 brachydanio
28	42	60.0	189	13	Q8QFN1	Q8qfn1 fugu rubrip
29	42	60.0	192	5	Q9W0H8	Q9w0h8 drosophila
30	42	60.0	193	5	Q96051	Q96051 drosophila
31	42	60.0	329	5	Q8SZK6	Q8szk6 drosophila
32	42	60.0	493	10	Q9ASV9	Q9asv9 arabidopsis
33	42	60.0	574	10	Q9MAH9	Q9mah9 arabidopsis
34	42	60.0	1636	16	Q9PEL7	Q9pel7 xylella fas
35	42	60.0	1779	5	Q9VM49	Q9vm49 drosophila
36	41	58.6	169	5	Q966R1	Q966r1 dictyosteli
37	41	58.6	231	16	Q98N90	Q98n90 rhizobium l
38	41	58.6	282	16	Q9PP67	Q9pp67 campylobact
39	41	58.6	322	5	Q93136	Q93136 bombyx mori
40	41	58.6	343	5	Q25793	Q25793 plasmodium
41	41	58.6	411	4	Q9P129	Q9p129 homo sapien
42	41	58.6	475	6	O18757	O18757 oryctolagus
43	41	58.6	571	5	Q966F0	Q966f0 caenorhabdi
44	41	58.6	576	5	Q9BIJ4	Q9bij4 caenorhabdi
45	41	58.6	589	5	Q9N5B9	Q9n5b9 caenorhabdi

ALIGNMENTS

RESULT 1

Q9HBZ8 PRELIMINARY; PRT; 328 AA.
AC Q9HBZ8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Reticulocabin.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HYPOPHALAMUS;
RA Peng Y., Gu Y., Huang C., Xu S., Han Z., Pu G., Chen Z.;
RT "A novel gene expressed in human hypothalamus.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183423; AAG09692.1; -
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; EF-hand.
DR Pfam; PF00036; ehand; 4.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00014; EF_TARGET; UNKNOWN_1.
SQ SEQUENCE 328 AA; 37424 MW; 9D23648795D3C670 CRC64;

Query Match

Best Local Similarity 100.0%; Score 70; DB 4; Length 328;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLGSGEV 13

|||||

Db 254 DLNKGHLGSGEV 266

RESULT 2

Q96D15

ID Q96D15 PRELIMINARY; PRT; 328 AA.

Tue May 20 14:43:33 2003

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AC Q96D15;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 37.5 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013436; AAH13436.1;
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 5.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 328 AA; 37493 MW; B64EDB28B9610B8D CRC64;

Query Match 100.0%; Score 70; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLGDSGV 13
DB 254 DLNKGHLGDSGV 266
|||||
RESULT 3
O9CTD4 PRELIMINARY; PRT; 259 AA.
AC Q9CTD4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 6030455P07RIK.
GN 6030455P07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo T., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Stauble F., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003918; BAB23076.1;
DR MGD; MGI:1915346; 6030455P07RIK.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER_target.
```

```
Pfam; PF00036; ehand; 4.
DR SMART; SM00054; EPH; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 259 AA; 31063 MW; 7910A9F0476260A1 CRC64;

Query Match 88.6%; Score 62; DB 11; Length 259;
Best Local Similarity 92.3%; Pred. No. 0.015;
Matches 12; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 1 DLNKGHLGDSGV 13
DB 185 DLNKGDLGDSGV 197
|||||
RESULT 4
Q99K35 PRELIMINARY; PRT; 315 AA.
AC Q99K35;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to hypothetical protein LOC57333 (Fragment).
GN 6030455P07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005487; AAH05487.1;
DR MGD; MGI:1915346; 6030455P07RIK.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00036; ehand; 4.
DR SMART; SM00054; EPH; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 315 AA; 36269 MW; CECB4DAEE54D24E4 CRC64;

Query Match 88.6%; Score 62; DB 11; Length 315;
Best Local Similarity 92.3%; Pred. No. 0.018;
Matches 12; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 1 DLNKGHLGDSGV 13
DB 241 DLNKGDLGDSGV 253
|||||
RESULT 5
Q8R137 PRELIMINARY; PRT; 328 AA.
AC Q8R137;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to hypothetical protein LOC57333.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025602; AAH25602.1;
KW Hypothetical protein.
SQ SEQUENCE 328 AA; 37973 MW; 913F5C6F0F88B316 CRC64;
```


Query Match 88.6%; Score 62; DB 11; Length 328;
 Best Local Similarity 92.3%; Pred. No. 0.019;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLNKGHLGSGSEV 13
 ||||| |||||
 DB 254 DLNKGHLGSGSEV 266

RESULT 6

ID Q96NQ4 PRELIMINARY; PRT; 384 AA.
 AC Q96NQ4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE CDNA FLJ30339 fis, clone BRACE2007401, moderately similar to
 DE Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier
 DE mRNA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CEREBELLUM;
 RA Toshiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
 RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hiro Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
 RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
 RA Isogai T.;
 RT "NEDO human cDNA sequencing project";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK054901; BAB70825.1;
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam; PF00036; efhand; 2.
 DR Pfam; PF00153; mito_carr; 3.
 DR ProDom; PD000012; EF-hand; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 SQ SEQUENCE 384 AA; 43018 MW; 33973A38D1F9BC5E CRC64;

Query Match 68.6%; Score 48; DB 4; Length 384;
 Best Local Similarity 61.5%; Pred. No. 5.3;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLGSGSEV 13
 |::|||:| |:
 DB 6 DRNQGHLIDVSEI 18

RESULT 7

Q9BV35
 ID Q9BV35 PRELIMINARY; PRT; 482 AA.
 AC Q9BV35;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 54.0 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EYE;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC001656; AAH01656.1;

DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002087; Mit_carrier.
 DR Pfam; PF00036; efhand; 3.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRODOM; PD000012; EF-hand; 1.
 DR SMART; SM00054; EPH; 3.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 482 AA; 54035 MW; 8917BEA2BC2FB42B CRC64;

Query Match 68.6%; Score 48; DB 4; Length 482;
 Best Local Similarity 61.5%; Pred. No. 6.7;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLGSGSEV 13
 |::|||:| |:
 DB 90 DRNQGHLIDVSEI 102

RESULT 8

Q91WH8
 ID Q91WH8 PRELIMINARY; PRT; 599 AA.
 AC Q91WH8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Similar to epidermal growth factor receptor pathway substrate 15,
 DE related sequence.
 GN EPS15-RS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015259; AAH15259.1;
 DR MGI; MGI:104582; Eps15-rs.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR000261; EPS15-repeat.
 DR Pfam; PF00036; efhand; 4.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 599 AA; 66206 MW; B62762A063F21FA9 CRC64;

Query Match 67.1%; Score 47; DB 11; Length 599;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLGSGSEV 12
 |::|||:| |:
 DB 172 DIDKGHLDRDE 183

RESULT 9

Q9UBC2
 ID Q9UBC2 PRELIMINARY; PRT; 864 AA.
 AC Q9UBC2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Epidermal growth factor receptor substrate EPS15R.
 GN EPS15R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

Tue May 20 14:43:33 2003

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RC TISSUE=BRAIN;
RA Nakashima S., Morinaka K., Ikeda M., Kishida S., Koyama S.,
RA Kikuchi A.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Ueki N.;
RT "HRI NTT human fetal brain cDNA Project.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF110265; AAF21930.1; -
DR EMBL; AB015346; BAA88118.1; -
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000261; EPS15_repeat.
DR Pfam; PF00036; ehand; 4.
DR SMART; SM00054; EFh; 3.
DR SMART; SM00027; EH; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 864 AA; 94254 MW; F4126069F6E00387 CRC64;

Query Match 67.1%; Score 47; DB 4; Length 864;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSE 12
Db 172 DIDKDGHLDRDE 183

RESULT 10
Q60902 PRELIMINARY; PRT; 907 AA.
AC Q60902;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-2002 (TrEMBLrel. 20, Last annotation update)
DE Eps15R protein.
GN EPS15-RS OR EPS15R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE;
RX MEDLINE=96003812; PubMed=7568168;
RA Wong W.T., Schumacher C., Salcini A.E., Romano A., Castagnino P.,
RA Pellicci P.G., Di Fiore P.;
RT "A protein-binding domain, EH, identified in the receptor tyrosine
RT kinase substrate Eps15 and conserved in evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9530-9534(1995).
DR MGD; U29156; AAA87202.1; -
DR MGD; MGI:104582; Eps15-rs.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000261; EPS15_repeat.
DR InterPro; IPR003903; UIM.
DR Pfam; PF00036; ehand; 4.
DR SMART; SM00054; EFh; 3.
DR SMART; SM00027; EH; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
SQ SEQUENCE 907 AA; 99320 MW; 2FA79DFB4C834E1E CRC64;

Query Match 67.1%; Score 47; DB 11; Length 907;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSE 12
Db 172 DIDKDGHLDRDE 183

RESULT 11
Q22159 PRELIMINARY; PRT; 127 AA.
AC Q22159;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE T04F3.4 protein.
GN T04F3.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kershaw J.K.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z72513; CAA96671.2; -
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
SQ SEQUENCE 127 AA; 14704 MW; 40CE9A863ADE694 CRC64;

Query Match 65.7%; Score 46; DB 5; Length 127;
Best Local Similarity 61.5%; Pred. No. 3.5;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSEV 13
Db 62 DLNKNFIDGIEI 74

RESULT 12
Q9PM44 PRELIMINARY; PRT; 289 AA.
AC Q9PM44;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein Cj1631c.
GN Cj1631c.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagsels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajadream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL; AL139079; CAB73619.1; -
DR InterPro; IPR02048; EF-hand.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 289 AA; 32539 MW; 98B618A0419F7BEC CRC64;

Query Match 64.3%; Score 45; DB 16; Length 289;
Best Local Similarity 61.5%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```


QY 1 DLNRDGHLDGSEV 13
 ID O93434 PRELIMINARY; PRT; 322 AA.
 Db 165 DVNRDGRVDDSDV 177

RESULT 13

AC O93434; PRELIMINARY; PRT; 322 AA.
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Reticulocalbin.
 GN RCN1.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Takifugu.
 OC NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99007268; PubMed=9789042;
 RA Miles C., Elgar G., Coles E., Kleinjan D.J., Van Heyningen V.,
 RA Hastie N.;
 RT "Complete sequencing of the Fugu WAGR region from Wt1 to Pax6:
 RT Dramatic compaction and conservation of synteny with human chromosome
 RT 1p13.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:13068-13072(1998).
 DR EMBL; AL021533; CAA16492.1; -;
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000886; EF-target.
 DR Pfam; PF00036; ehand; 6.
 DR SMART; SM00054; Efh; 2.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
 DR PROSITE; PS00014; EF_TARGET; UNKNOWN_1.
 SQ SEQUENCE 322 AA; 38207 MW; 85F99C053AC34C5C CRC64;

Query Match 62.9%; Score 44; DB 13; Length 322;
 Best Local Similarity 61.5%; Pred. No. 21;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNRDGHLDGSEV 13
 ID O90460 PRELIMINARY; PRT; 343 AA.
 Db 248 DLNRDGRVDDSDV 260

RESULT 14

AC O90460; PRELIMINARY; PRT; 343 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Membrane-associated calcium-binding protein.
 GN PFS40.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OC NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FCCL/RN;
 RA Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M.;
 RT "Construction of a prokaryotic expression plasmid and sequence
 RT analysis of the pfs40 gene of Plasmodium falciparum HAINAN isolate.";
 RL Chung-Kuo Jen Shou Kung Huan Ping Tsa Chih 17:21-25(2001).
 DR EMBL; AF202094; AAF14633.1; -;
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 5.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; Efh; 5.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_5.
 SQ SEQUENCE 343 AA; 39421 MW; A0F59D86D070529E CRC64;

Query Match 62.9%; Score 44; DB 5; Length 343;
 Best Local Similarity 53.8%; Pred. No. 22;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNRDGHLDGSEV 13
 Db 223 DLNRDGRVDDSDV 235

RESULT 15

AC O90460; PRELIMINARY; PRT; 592 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE PHA synthase.
 GN PHACRR.
 OS Rhodospirillum rubrum.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
 OC Rhodospirillum.
 OC NCBI_TaxID=1085;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20261043; PubMed=10803898;
 RA Clemente T., Shah D., Tran M., Stark D., Padgett S., Dennis D.,
 RA Brueckner K., Steinbuechel A., Mitsky T.;
 RT "Sequence of PHA synthase gene from two strains of Rhodospirillum
 RT rubrum and in vivo substrate specificity of four PHA synthases across
 RT two heterologous expression systems.";
 RL Appl. Microbiol. Biotechnol. 53:420-429(2000).
 DR EMBL; AJ245888; CAB65395.1; -;
 SQ SEQUENCE 592 AA; 66428 MW; 87A254102DC5675F CRC64;

Query Match 62.9%; Score 44; DB 2; Length 592;
 Best Local Similarity 66.7%; Pred. No. 40;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DLNRDGHLDGSEV 13
 Db 388 DLNRDGRVDDSDV 399

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 Job time : 6.1173 secs

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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:41:13 ; Search time 1.4868 Seconds
(without alignments)
257.262 Million cell updates/sec

Title: US-09-768-840-1_COPY_254_266

Perfect score: 70
Sequence: 1 DLNKGHLGSEV 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	328	2	US-08-828-242-1
2	70	100.0	328	2	US-08-910-927B-1
3	70	100.0	328	4	US-09-206-493-1
4	70	100.0	328	4	US-09-270-270-1
5	48	68.6	325	2	US-08-828-242-4
6	48	68.6	325	4	US-09-206-499-4
7	48	68.6	331	2	US-08-828-242-3
8	48	68.6	331	2	US-08-910-927B-5
9	48	68.6	331	4	US-09-206-499-3
10	48	68.6	331	4	US-09-270-270-5
11	40	57.1	203	4	US-09-399-913-12
12	40	57.1	203	4	US-09-399-913-12
13	40	57.1	216	4	US-09-399-913-2
14	40	57.1	216	4	US-09-399-913-6
15	40	57.1	216	4	US-09-298-731-2
16	40	57.1	216	4	US-09-298-731-6
17	40	57.1	227	4	US-09-399-913-8
18	40	57.1	227	4	US-09-399-913-8
19	40	57.1	227	4	US-09-298-731-8
20	40	57.1	227	4	US-09-298-731-10
21	40	57.1	245	4	US-09-399-913-4
22	40	57.1	245	4	US-09-298-731-4
23	40	57.1	3969	4	US-08-061-377-5
24	39	55.7	105	2	US-08-918-726-6
25	39	55.7	105	3	US-09-205-680A-6
26	39	55.7	276	3	US-09-048-889-4
27	39	55.7	313	4	US-09-134-001C-4371

28	39	55.7	473	1	US-08-073-383-6	Sequence 6, Appli
29	39	55.7	473	5	PCT-US94-06365-6	Sequence 6, Appli
30	38	54.3	109	4	US-09-399-913-34	Sequence 34, Appli
31	38	54.3	109	4	US-09-298-731-34	Sequence 3, Appli
32	38	54.3	188	3	US-09-048-889-3	Sequence 32, Appli
33	38	54.3	200	4	US-09-298-731-32	Sequence 70, Appli
34	38	54.3	229	4	US-09-399-913-70	Sequence 49, Appli
35	38	54.3	233	4	US-09-399-913-49	Sequence 51, Appli
36	38	54.3	233	4	US-09-399-913-51	Sequence 9, Appli
37	38	54.3	246	1	US-08-271-354-9	Sequence 9, Appli
38	38	54.3	246	2	US-08-565-861-9	Sequence 9, Appli
39	38	54.3	246	5	PCT-US94-07658-9	Sequence 9, Appli
40	38	54.3	250	4	US-09-399-913-72	Sequence 72, Appli
41	38	54.3	256	4	US-09-399-913-32	Sequence 32, Appli
42	37	52.9	837	4	US-09-390-234-14	Sequence 14, Appli
43	36	51.4	12	5	PCT-US93-05701-11	Sequence 11, Appli
44	36	51.4	20	1	US-07-740-175B-5	Sequence 5, Appli
45	36	51.4	20	5	PCT-US92-06334A-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-828-242-1
; Sequence 1, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CONUTUT01
; CLONE: 2509570
US-08-828-242-1

Query Match 100.0%; Score 70; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13
 Db 254 DLNKGHLGSEV 266

RESULT 2
 US-08-910-927B-1
 ; Sequence 1, Application US/08910927B
 ; Patent No. 5976801
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/910,927B
 ; FILING DATE: Hereewith
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0358 US
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 328 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: RATNOT02
 ; CLONE: 922578
 ; US-08-910-927B-1

Query Match 100.0%; Score 70; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13
 Db 254 DLNKGHLGSEV 266

RESULT 3
 US-09-206-499-1
 ; Sequence 1, Application US/09206499
 ; Patent No. 6194385
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: NOVEL CALCIUM-BINDING

; TITLE OF INVENTION: PROTEIN
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/206,499
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/828,242
 ; FILING DATE: 03/31/1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0261 US
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 328 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: CONUTUT01
 ; CLONE: 2509570
 ; US-09-206-499-1

Query Match 100.0%; Score 70; DB 4; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13
 Db 254 DLNKGHLGSEV 266

RESULT 4
 US-09-270-270-1
 ; Sequence 1, Application US/09270270
 ; Patent No. 6235477
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/270,270
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/910,927
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0358 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: RAYNOT02
CLONE: 922578
US-09-270-270-1

Query Match 100.0%; Score 70; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13
DB 254 DLNKGHLGSEV 266

RESULT 5

US-08-828-242-4
Sequence 4, Application US/08828242
Patent No. 5871970
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL CALCIUM-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,242
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0261 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 220582
US-08-828-242-4

Query Match 68.6%; Score 48; DB 2; Length 325;
Best Local Similarity 69.2%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13
DB 251 DLNKGKLDKDEI 263

RESULT 6

US-09-206-499-4
Sequence 4, Application US/09206499
Patent No. 6194385
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL CALCIUM-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,499
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,242
FILING DATE: 03/31/1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0261 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 220582
US-09-206-499-4

Query Match 68.6%; Score 48; DB 4; Length 325;
Best Local Similarity 69.2%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13
DB 251 DLNKGKLDKDEI 263

RESULT 7
US-08-828-242-3
; Sequence 3, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1262329
US-08-828-242-3

Query Match 68.6%; Score 48; DB 2; Length 331;
Best Local Similarity 69.2%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DLNKGHLDSGV 13
Db 257 DLNKGKLDKDEI 269

RESULT 8
US-08-910-927B-5
; Sequence 5, Application US/08910927B
; Patent No. 5976801
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,927B
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0358 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1262329
US-08-910-927B-5

Query Match 68.6%; Score 48; DB 2; Length 331;
Best Local Similarity 69.2%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DLNKGHLDSGV 13
Db 257 DLNKGKLDKDEI 269

RESULT 9
US-09-206-499-3
; Sequence 3, Application US/09206499
; Patent No. 6194385
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/206,499
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,242
; FILING DATE: 03/31/1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0261 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1262329
US-09-206-499-3

Query Match 68.6%; Score 48; DB 4; Length 331;
Best Local Similarity 69.2%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13
DB 257 DLNKGKLDKDEI 269

RESULT 10
US-09-270-270-5
Sequence 5, Application US/09270270
Patent No. 6235477
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,270
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/910,927
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0358 US
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1262329

US-09-270-270-5

Query Match 68.6%; Score 48; DB 4; Length 331;
Best Local Similarity 69.2%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13
DB 257 DLNKGKLDKDEI 269

RESULT 11
US-09-399-913-12
Sequence 12, Application US/09399913
Patent No. 6361971
GENERAL INFORMATION:
APPLICANT: Rhodes, Kenneth
APPLICANT: Betty, Maria
APPLICANT: Ling, Huai-Ping
APPLICANT: Ao, Wenqian
TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
FILE REFERENCE: MNI-070CP2
CURRENT APPLICATION NUMBER: US/09/399,913
CURRENT FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER: USSN 60/110,277
EARLIER FILING DATE: 1998-11-30
EARLIER APPLICATION NUMBER: USSN 60/110,033
EARLIER FILING DATE: 1998-11-25
EARLIER APPLICATION NUMBER: USSN 60/109,333
EARLIER FILING DATE: 1998-11-20
EARLIER APPLICATION NUMBER: USSN 09/298,731
EARLIER FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: USSN 09/350,614
EARLIER FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: USSN 09/350,874
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 203
TYPE: PRT
ORGANISM: Rattus sp.
US-09-399-913-12

Query Match 57.1%; Score 40; DB 4; Length 203;
Best Local Similarity 46.2%; Pred. No. 17;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13
DB 151 DINKGYINKKEEM 163

RESULT 12
US-09-298-731-12
Sequence 12, Application US/09298731
Patent No. 6369197
GENERAL INFORMATION:
APPLICANT: KENNETH RHODES, MARIA BETTY, HUAI-PING LING, AND FRANK AN
TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
FILE REFERENCE: MNI-070
CURRENT APPLICATION NUMBER: US/09/298,731
CURRENT FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 203
TYPE: PRT
ORGANISM: Rattus sp.
US-09-298-731-12

Query Match 57.1%; Score 40; DB 4; Length 203;
Best Local Similarity 46.2%; Pred. No. 17;

Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
|:|||||::|:
Db 151 DINKDGYINKEEM 163

RESULT 13
US-09-399-913-2
; Sequence 2, Application US/09399913
; Patent No. 6361971
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: Betty, Maria
; APPLICANT: Ling, Huai-Ping
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
; FILE REFERENCE: MNI-070CP2
; CURRENT APPLICATION NUMBER: US/09/399,913
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: USSN 09/350,614
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 09/350,874
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-399-913-2

Query Match 57.1%; Score 40; DB 4; Length 216;
Best Local Similarity 46.2%; Pred. No. 18;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
|:|||||::|:
Db 135 DINKDGYINKEEM 147

RESULT 14
US-09-399-913-6
; Sequence 6, Application US/09399913
; Patent No. 6361971
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: Betty, Maria
; APPLICANT: Ling, Huai-Ping
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
; FILE REFERENCE: MNI-070CP2
; CURRENT APPLICATION NUMBER: US/09/399,913
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: USSN 09/350,614
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 09/350,874

; EARLIER FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-399-913-6

Query Match 57.1%; Score 40; DB 4; Length 216;
Best Local Similarity 46.2%; Pred. No. 18;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
|:|||||::|:
Db 135 DINKDGYINKEEM 147

RESULT 15
US-09-298-731-2
; Sequence 2, Application US/09298731
; Patent No. 6369197
; GENERAL INFORMATION:
; APPLICANT: KENNETH RHODES, MARIA BETTY, HUAI-PING LING, AND FRANK AN
; TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
; FILE REFERENCE: MNI-070
; CURRENT APPLICATION NUMBER: US/09/298,731
; CURRENT FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-298-731-2

Query Match 57.1%; Score 40; DB 4; Length 216;
Best Local Similarity 46.2%; Pred. No. 18;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
|:|||||::|:
Db 135 DINKDGYINKEEM 147

Search completed: May 14, 2003, 10:47:15
Job time : 2.4868 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:34:02 ; Search time 4.1173 Seconds
(without alignments)
420.726 Million cell updates/sec

Title: US-09-768-840-1_copy_254_266
Perfect score: 70
Sequence: 1 DLNKGHLGSEV 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	ID	Description
1	70	100.0	240	22	AAG75587	Human colon cancer
2	70	100.0	328	19	AAW80746	Human calcium-bind
3	70	100.0	328	20	AAI13382	Amino acid sequenc
4	70	100.0	328	20	AAI00916	Human reticulocalb
5	70	100.0	328	20	AAW67852	Human secreted pro
6	70	100.0	328	21	AAW33424	Human PRO272 prote
7	70	100.0	328	21	AAI53640	A bone marrow secr
8	70	100.0	328	22	AAI12353	Human PRO272 polyp
9	70	100.0	328	22	AAG64865	Human calcium bind
10	70	100.0	328	22	AAW80250	Human PRO272 prote

11	70	100.0	328	22	AAB53085	Human angiogenesis
12	70	100.0	343	22	AAU87402	Novel central nerv
13	70	100.0	343	22	AAW43584	Human polypeptide
14	70	100.0	343	22	AAU19946	Novel human calciu
15	48	68.6	66	22	ABB27587	Human human calciu
16	48	68.6	66	22	ABB32751	Human peptide #238
17	48	68.6	66	22	ABB18233	Peptide #257 encod
18	48	68.6	66	22	AAW53562	Protein #232 encod
19	48	68.6	66	22	AAW65945	Human brain expres
20	48	68.6	66	22	AAW13812	Human bone marrow
21	48	68.6	66	22	AAW26213	Peptide #246 encod
22	48	68.6	66	22	AAW01556	Peptide #250 encod
23	48	68.6	66	23	ABG35583	Peptide #238 encod
24	48	68.6	311	23	ABP41959	Human peptide enco
25	48	68.6	325	22	AAG64867	Human ovarian anti
26	48	68.6	331	22	AAG64866	Murine reticulocalb
27	48	68.6	331	23	AAQ17363	Human reticulocalb
28	48	68.6	392	23	AAW47870	Human transporter
29	48	68.6	461	22	AAG65800	Human membrane tra
30	48	68.6	468	23	AAE22927	Human transporter
31	48	68.6	471	22	AAU27697	Human full-length
32	48	68.6	508	22	ABG22637	Novel human diagno
33	48	68.6	509	22	AAU27869	Human contig polyp
34	47	67.1	211	22	ABG05519	Novel human diagno
35	47	67.1	754	22	AAW95697	Human protein sequ
36	47	67.1	864	22	AAW40292	Human polypeptide
37	47	67.1	866	21	AAW86194	Nuclear transport
38	43	61.4	69	22	ABB29676	Peptide #2327 enco
39	43	61.4	69	22	ABB34856	Peptide #2362 enco
40	43	61.4	69	22	ABB20272	Protein #2271 enco
41	43	61.4	69	22	AAW53662	Human brain expres
42	43	61.4	69	22	AAW68044	Human bone marrow
43	43	61.4	69	22	AAW15863	Peptide #2297 enco
44	43	61.4	69	22	AAW22089	Peptide #8523 enco
45	43	61.4	69	22	AAW28371	Peptide #2408 enco

ALIGNMENTS

RESULT 1
AAG75587
ID AAG75587 standard; Protein; 240 AA.
XX
AC AAG75587;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:6351.
XX
KW Human; colon cancer; colon cancer,antigen; diagnosis; detection;
KW colorectal carcinoma.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
(HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
XX
PT N-PSDB; AAH34992.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -

XX PS Claim 11; Page 7803-7804; 9803pp; English.

XX CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon

XX CC cancer-associated nucleic acid molecules (N) and proteins (P), where

XX CC the proteins are collectively known as colon cancer antigens. The colon

XX CC cancer antigens have cytostatic activity and can be used in gene

XX CC therapy and vaccine production. N and P may be used in the prevention,

XX CC diagnosis and treatment of diseases associated with inappropriate P

XX CC expression. For example, N and P may be used to treat disorders

XX CC associated with decreased expression by rectifying mutations or deletions

XX CC in a patient's genome that affect the activity of P by expressing

XX CC inactive proteins or to supplement the patient's own production of P.

XX CC Additionally, N may be used to produce the colon cancer-associated P,

XX CC by inserting the nucleic acids into a host cell and culturing the cell

XX CC to express the proteins. N and P can be used in the prevention, diagnosis

XX CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204

XX CC and AAH77789 represent sequences used in the exemplification of the

XX CC present invention.

XX CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were

XX CC missing at time of publication, meaning no sequences are present for

XX CC SEQ ID NO:1027 to 1052, 7921 and 7922.

XX SQ Sequence 240 AA;

Query Match 100.0%; Score 70; DB 22; Length 240;

Best Local Similarity 100.0%; Pred. No. 0.00039;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSEV 13

Db 166 DLNKGHLDGSEV 178

RESULT 2

AAW80746

ID AAW80746 standard; Protein; 328 AA.

XX AC AAW80746;

XX DT 15-DEC-1998 (first entry)

XX DE Human calcium-binding protein.

XX KW Human; calcium-binding protein; reticulocalbin; sickle cell anaemia;

XX KW HCBP; beta thalassaemia; cell proliferation; cancer; adenocarcinoma;

XX KW leukemia; lymphoma; melanoma; sarcoma.

XX OS Homo sapiens.

XX PN WO9844114-A1.

XX PD 08-OCT-1998.

XX PF 30-MAR-1998; 98WO-US062233.

XX PR 31-MAR-1997; 97US-0828242.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Goli SK, Hillman JL;

XX DR WPI; 1998-542704/46.

XX DR N-PSDB; AAV57600.

XX PT A new human calcium binding protein - useful for treating or

XX PT preventing disorders associated with the expression of HCBP

XX PS Claim 1; Page 42-43; 60pp; English.

XX CC The present sequence is a new human calcium binding protein (HCBP).

XX CC A pharmaceutical composition which includes the HCBP protein is claimed

XX CC and can be added directly to cells in vivo to promote regeneration or

CC differentiation of cells. HCBP can also be added to cells, cell lines,

CC tissue or organ culture to stimulate cell proliferation for heterologous

CC and autologous transplantation. The cells can be selected for their

CC ability to inhibit development of an infection or to correct a genetic

CC defect such as sickle cell anaemia, beta thalassaemia. An antagonist of

CC HCBP can be administered to a subject to treat or prevent a disorder

CC associated with cell proliferation e.g. many cancers including

CC adenocarcinoma, leukemia, lymphoma, melanoma, sarcoma and particularly

CC cancers of bladder, bone, brain, heart, kidney, liver. Antibodies

CC specific for HCBP may be used directly as an antagonist or indirectly as

CC a targeting or delivery mechanism for delivering pharmaceutical agents

CC to cell or tissue which express protein HCBP. A method is claimed for

CC treating or preventing a disorder associated with cell proliferation

CC which involves adding pharmaceutical composition of antagonist of HCBP.

XX SQ Sequence 328 AA;

Query Match 100.0%; Score 70; DB 19; Length 328;

Best Local Similarity 100.0%; Pred. No. 0.00056;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSEV 13

Db 254 DLNKGHLDGSEV 266

RESULT 3

AAV13382

ID AAV13382 standard; Protein; 328 AA.

XX AC AAV13382;

XX DT 25-JUN-1999 (first entry)

XX DE Amino acid sequence of protein PRO272.

XX KW Secreted protein; transmembrane protein; human; enterocolitis;

XX KW Zollinger-Ellison syndrome; gastrointestinal ulceration;

XX KW congenital microvillus atrophy; skin disease; cell growth;

XX KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;

XX KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;

XX KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;

XX KW anti-thrombotic; wound healing; tissue repair.

XX OS Homo sapiens.

XX PN WO9914328-A2.

XX PD 25-MAR-1999.

XX PF 16-SEP-1998; 98WO-US19330.

XX PR 25-NOV-1997; 97US-0066840.

XX PR 17-SEP-1997; 97US-0059113.

XX PR 17-SEP-1997; 97US-0059115.

XX PR 17-SEP-1997; 97US-0059117.

XX PR 17-SEP-1997; 97US-0059119.

XX PR 17-SEP-1997; 97US-0059121.

XX PR 17-SEP-1997; 97US-0059122.

XX PR 17-SEP-1997; 97US-0059184.

XX PR 18-SEP-1997; 97US-0059263.

XX PR 18-SEP-1997; 97US-0059266.

XX PR 15-OCT-1997; 97US-0062125.

XX PR 17-OCT-1997; 97US-0062285.

XX PR 21-OCT-1997; 97US-0063486.

XX PR 24-OCT-1997; 97US-0062814.

XX PR 24-OCT-1997; 97US-0062816.

XX PR 24-OCT-1997; 97US-0063045.

XX PR 24-OCT-1997; 97US-0063120.

XX PR 24-OCT-1997; 97US-0063121.

XX PR 24-OCT-1997; 97US-0063127.

XX PR 24-OCT-1997; 97US-0063128.

PR 27-OCT-1997; 97US-0063329.
 PR 27-OCT-1997; 97US-0063327.
 PR 28-OCT-1997; 97US-0063541.
 PR 28-OCT-1997; 97US-0063542.
 PR 28-OCT-1997; 97US-0063544.
 PR 28-OCT-1997; 97US-0063549.
 PR 28-OCT-1997; 97US-0063550.
 PR 28-OCT-1997; 97US-0063564.
 PR 29-OCT-1997; 97US-0063435.
 PR 29-OCT-1997; 97US-0063704.
 PR 29-OCT-1997; 97US-0063732.
 PR 29-OCT-1997; 97US-0063738.
 PR 29-OCT-1997; 97US-0063734.
 PR 29-OCT-1997; 97US-0064215.
 PR 31-OCT-1997; 97US-0063735.
 PR 31-OCT-1997; 97US-0063870.
 PR 31-OCT-1997; 97US-0064103.
 PR 03-NOV-1997; 97US-0064248.
 PR 07-NOV-1997; 97US-0064809.
 PR 12-NOV-1997; 97US-0065186.
 PR 17-NOV-1997; 97US-0065846.
 PR 18-NOV-1997; 97US-0065693.
 PR 21-NOV-1997; 97US-0066120.
 PR 21-NOV-1997; 97US-0066364.
 PR 24-NOV-1997; 97US-0066772.
 PR 24-NOV-1997; 97US-0066466.
 PR 24-NOV-1997; 97US-0066770.
 PR 24-NOV-1997; 97US-0066511.
 PR 24-NOV-1997; 97US-0066453.
 PA (GETH) GENENTECH INC.
 XX
 XX
 XX
 PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
 DR WPI; 1999-229533/19.
 DR N-PSDB; AAX52253.
 XX
 XX New isolated human genes and polypeptides used in, e.g. treatment of
 gastrointestinal ulceration
 XX
 XX Claim 12; Fig 80; 320pp; English.
 XX
 XX AAY13344-403 represent secreted and transmembrane human proteins.
 CC The cDNA sequences are obtained from cDNA libraries, prepared from
 CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
 CC The encoded polypeptides have specific uses based on their homology to
 CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders
 CC associated with the preservation and maintenance of gastrointestinal
 CC mucosa and the repair of acute and chronic mucosal lesions
 CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
 CC ulceration and congenital microvillus atrophy), skin diseases associated
 CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
 CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),
 CC potent effects on cell growth and development, diseases related to
 CC growth or survival of nerve cells including Parkinson's disease,
 CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as
 CC for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used
 CC as a target for anti-tumor drugs. PRO533 may be used in the treatment
 CC of Usher Syndrome or Atrophia areata; PRO269 can be used as an
 CC anti-thrombotic agent; PRO287 polypeptides and portions may have
 CC therapeutic applications in wound healing and tissue repair; PRO317 can
 CC be used for treating problems of the kidney, uterus, endometrium, blood
 CC vessels, or related tissue, e.g. in the heart of genital tract.
 XX
 XX Sequence 328 AA;

Query Match 100.0%; Score 70; DB 20; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00056;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DLNKGHLGDSGV 13
 Db 254 DLNKGHLGDSGV 266

RESULT 4
 AAY00916
 ID AAY00916 standard; Protein; 328 AA.
 XX
 AC AAY00916;
 XX
 DT 28-MAY-1999 (first entry)
 XX
 DE Human reticulocalbin gamma protein sequence.
 XX
 KW Human; reticulocalbin gamma; RCNgamma; reticulocalbin delta; RCNdelta;
 KW developmental disorder; neoplastic disorder; immunological disorder;
 XX infection.
 XX
 OS Homo sapiens.
 XX
 PN WO9907849-A2.
 XX
 PD 18-FEB-1999.
 XX
 PF 05-AUG-1998; 98WO-US16259.
 XX
 PR 08-AUG-1997; 97US-0910927.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Bandman O, Corley NC, Hillman JL, Lal P, Shah P;
 DR WPI; 1999-180492/15.
 DR N-PSDB; AAX27229.
 XX
 PT New human reticulocalbin isoforms - useful to diagnose, prevent,
 PT and treat infectious, developmental, neoplastic, and immunological
 PT disorders
 XX
 PS Claim 1; Fig 1; 82pp; English.

CC This sequence is the human reticulocalbin gamma (RCNgamma) of the
 CC invention. RCNgamma and RCNdelta are used to treat an infectious or
 CC developmental disorder, and antagonists of them are used to treat a
 CC neoplastic or immunological disorder. Infectious disorders include e.g.
 CC pneumonia, lymphocytic choriomeningitis, Hantavirus, chronic bronchitis,
 CC hepatitis, herpesviruses, yellow fever, influenza, cancer, measles,
 CC mumps, rhinovirus, poliovirus, coxsackie-virus, smallpox, Colorado tick
 CC fever, HIV, rabies, gastroenteritis, and rubella, encephalitis, and
 CC bacterial, fungal, parasitic, protozoal, or helminthic infections.
 CC Developmental disorders include e.g. renal tubular acidosis, anaemia,
 CC Cushing's syndrome, achondroplastic dwarfism, epilepsy, gonadal
 CC dysgenesis, hereditary neuropathies such as Charcot-Marie-Tooth disease,
 CC and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders
 CC such as Sydenham's chorea and cerebral palsy, spinal bifida, and
 CC congenital glaucoma, cataract, or sensorineural hearing loss. Neoplastic
 CC disorders include e.g. adenocarcinoma, leukaemia, lymphoma, melanoma,
 CC myeloma, sarcoma and teratocarcinoma. Overexpression of reticulocalbin
 CC mRNA has been associated with increased metastatic invasive properties of
 CC three human breast cancer lines.

CC Sequence 328 AA;
 Query Match 100.0%; Score 70; DB 20; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00056;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DLNKGHLGDSGV 13
 Db 254 DLNKGHLGDSGV 266

RESULT 5
 AAW67852
 ID AAW67852 standard; Protein; 328 AA.

CC The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological CC conditions can be diagnosed by determining the amount of the new CC polypeptides in a sample or by determining the presence of mutations in CC the new polynucleotides. Specific uses are described for each of the 87 CC polynucleotides, based on which tissues they are most highly expressed in CC (see AAX00611 for described uses).

XX Sequence 328 AA;
SQ Query Match 100.0%; Score 70; DB 20; Length 328;
Best Local Similarity 100.0%; Pred. NO. 0.00056; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

QY 1 DLNKGHLDGSEV 13
DB 253 DLNKGHLDGSEV 265
|||||

RESULT 6
AAB33424
ID AAB33424 standard; Protein; 328 AA.
XX AC. AAB33424;
XX DT 29-JAN-2001 (first entry)
XX DE Human PRO272 protein UNQ239 SEQ ID NO:51.
XX KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; neutropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW inflammatory disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX Homo sapiens.
OS
XX WO200053758-A2.
XX PN
XX PD 14-SEP-2000.
XX PF 02-MAR-2000; 2000WO-US05841.
XX PR 08-MAR-1999; 99WO-US05028.
XX PR 10-MAR-1999; 99US-0123618.
XX PR 12-MAR-1999; 99US-0123957.
XX PR 23-MAR-1999; 99US-0125775.
XX PR 12-APR-1999; 99US-0128849.
XX PR 28-APR-1999; 99WO-US08615.
XX PR 20-MAY-1999; 99US-0131445.
XX PR 04-MAY-1999; 99US-0132371.
XX PR 14-MAY-1999; 99US-0134287.
XX PR 02-JUN-1999; 99WO-US12252.
XX PR 23-JUN-1999; 99US-0141037.
XX PR 20-JUL-1999; 99US-0144758.
XX PR 26-JUL-1999; 99US-0145698.
XX PR 28-JUL-1999; 99US-0146222.
XX PR 01-SEP-1999; 99WO-US20111.
XX PR 08-SEP-1999; 99WO-US20594.
XX PR 13-SEP-1999; 99WO-US20944.
XX PR 15-SEP-1999; 99WO-US21090.
XX PR 15-SEP-1999; 99WO-US21547.

XX AAW67852;
XX 25-MAR-1999 (first entry)
XX Human secreted protein encoded by gene 46 clone HSJBQ79.
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
XX Misc-difference 300
XX /label= unknown
XX Misc-difference 328
XX /label= unknown
XX WO9842738-A1.
XX 01-OCT-1998.
XX 19-MAR-1998; 98WO-US05311.
XX 30-MAY-1997; 97US-0050937.
XX 21-MAR-1997; 97US-0041276.
XX 21-MAR-1997; 97US-0041277.
XX 21-MAR-1997; 97US-0041281.
XX 21-MAR-1997; 97US-0042344.
XX 30-MAY-1997; 97US-0048069.
XX 30-MAY-1997; 97US-0048094.
XX 30-MAY-1997; 97US-0048095.
XX 30-MAY-1997; 97US-0048096.
XX 30-MAY-1997; 97US-0048099.
XX 30-MAY-1997; 97US-0048131.
XX 30-MAY-1997; 97US-0048135.
XX 30-MAY-1997; 97US-0048154.
XX 30-MAY-1997; 97US-0048160.
XX 30-MAY-1997; 97US-0048186.
XX 30-MAY-1997; 97US-0048187.
XX 30-MAY-1997; 97US-0048188.
XX 30-MAY-1997; 97US-0048350.
XX 30-MAY-1997; 97US-0048351.
XX 30-MAY-1997; 97US-0048352.
XX 30-MAY-1997; 97US-0048355.
XX 05-AUG-1997; 97US-0054804.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;
XX Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;
XX Rosen CA, Ruben SM, Shi Y, Young P;
XX WPI; 1999-070066/06.
XX N-PSDB; AAX00636.
XX New isolated human genes and the secreted polypeptides they encode -
XX useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders
XX Claim 11; Page 297-298; 385pp; English.
XX This sequence represents a secreted human protein encoded by the gene
XX clone detailed in the descriptor line. The gene can be used to generate
XX fusion proteins by linking to the gene to a human immunoglobulin Fc
XX portion (e.g. AAX00602) for increasing the stability of the fused
XX protein as compared to the human protein only.

PR 05-OCT-1999; 99WO-US23089.
 PR 29-OCT-1999; 99US-0162506.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 16-DEC-1999; 99WO-US28585.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 11-FEB-2000; 2000WO-US00376.
 PR 18-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
 XX
 DR WPI: 2000-572271/53.
 DR N-PSDB; AAC58589.
 XX
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
 XX
 XX Claim 33; Fig 22; 309pp; English.
 XX
 CC The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC and peripheral nervous systems, demyelinating diseases of the central,
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
 CC autoimmune or immune-mediated skin diseases, allergic diseases,
 CC immunological diseases of the lung, and transplantation associated
 CC diseases including graft rejection and graft-versus-host-disease.
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 XX Sequence 328 AA;
 XX
 Query Match 100.0%; Score 70; DB 21; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00056;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLNKGDLGDSGV 13
 |||||
 Db 254 DLNKGDLGDSGV 266
 RESULT 7
 ID AAY53640
 XX AAY53640 standard; Protein: 328 AA.
 AC AAY53640;
 XX

DT 22-FEB-2000 (first entry)
 XX A bone marrow secreted protein designated BMS37.
 DE
 XX
 KW Bone marrow secreted protein; bone marrow stromal cell; cytokine;
 KW cell proliferation; cell differentiation; hematopoiesis; anaemia;
 KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
 KW erythroid progenitor cell; colony stimulating factor; granulocyte;
 KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
 KW platelet disorder; thrombocytopenia; hematopoietic stem cell;
 KW stem cell disorder; aplastic anaemia; bone differentiation;
 KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage;
 KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
 KW bone fracture; cartilage damage; artificial joint.
 XX Homo sapiens.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "signal peptide"
 XX
 XX WO9933979-A2.
 XX
 PD 08-JUL-1999.
 XX
 PF 18-DEC-1998; 98WO-US27008.
 XX
 PR 30-DEC-1997; 97US-0068958.
 PR 24-SEP-1998; 98US-0101603.
 PR 30-SEP-1998; 98US-0102540.
 XX
 XX (CHIR) CHIRON CORP.
 XX
 PI Lin H, Cao L;
 PI
 DR WPI: 2000-038344/03.
 DR N-PSDB; AAZ36246.
 XX
 PT New isolated human polynucleotide and secreted proteins can induce
 PT production of other cytokines in certain cell populations -
 XX
 PS Claim 2; Page 113; 120pp; English.
 XX
 CC AAY53622-43 represent bone marrow secreted proteins of human bone marrow
 CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or
 CC cell differentiation activity (either inducing or inhibiting). They can
 CC be used to support colony forming cells or factor-dependent cell lines,
 CC to regulate hematopoiesis, and to treat myeloid or lymphoid cell
 CC deficiencies. In addition, they may be used to support the growth and
 CC proliferation of erythroid progenitor cells, and to treat various
 CC anaemias. They can have colony stimulating factor (CSF) activity and can
 CC be used to support the growth and proliferation of myeloid cells such as
 CC granulocytes, monocytes or macrophages, to prevent or treat
 CC megakaryocytes and platelets, thereby allowing prevention or treatment
 CC of platelet disorders such as thrombocytopenia, to support the growth
 CC and proliferation of hematopoietic stem cells, either in place of or in
 CC conjunction with platelet transfusions, to treat stem cell disorders,
 CC such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to
 CC repopulate the stem cell compartment after irradiation or chemotherapy.
 CC They can be used for growth or differentiation of bone, cartilage,
 CC tendon, ligament, or nerve tissue, as well as for wound healing and
 CC tissue repair and replacement, and in the treatment of burns, incisions
 CC and ulcers, to induce cartilage and/or bone growth in circumstances
 CC where bone is not normally formed and thus have an application in healing
 CC bone fractures and cartilage damage or defects, prophylactic use in
 CC fracture reduction and also in the improved fixation of artificial
 CC joints.
 XX
 XX Sequence 328 AA;
 XX
 Query Match 100.0%; Score 70; DB 21; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00056;

CC diagnosis, prevention and treatment of cell proliferation disorders, such
 CC as cancer. The present sequence is the protein of the invention.

XX Sequence 328 AA;

Query Match 100.0%; Score 70; DB 22; Length 328;

Best Local Similarity 100.0%; Pred. No. 0.00056;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13

|||||

Db 254 DLNKGHLGSEV 266

RESULT 10

AA80250

ID AAB80250 standard; Protein; 328 AA.

XX

AC AAB80250;

XX 24-APR-2001 (first entry)

DT Human PRO272 protein.

DE

XX Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;

KW antiparkinsonian nootropic; neuroprotective; vulnery; cardiant;

KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;

KW antiarthritic; antifertility; antidiabetic; antiviral; diabetes;

KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;

XX ischaemia; inflammation.

XX

OS Homo sapiens.

XX

PN WO200104311-A1.

XX 18-JAN-2001.

PD

XX

XX 22-FEB-2000; 2000WO-US04414.

XX

PR 07-JUL-1999; 99US-0143048.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 08-SEP-1999; 99WO-US20594.

PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 05-OCT-1999; 99WO-US23089.

PR 29-NOV-1999; 99WO-US28214.

PR 30-NOV-1999; 99WO-US28313.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 05-JAN-2000; 99WO-US30599.

XX

PA (GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;

PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

PI Williams PM, Wood WI;

DR WPI: 2001-081051/09.

DR N-PSDB; AAF72411.

XX

PT Sixty one nucleic acids encoding PRO polypeptides which are useful in

PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung

PT squamous cell carcinoma) and neurodegenerative diseases (e.g.

PT Alzheimer's disease)

XX

PS Claim 1; Fig 80; 393pp; English.

XX

CC The present sequence is one of sixty one novel secreted and

CC transmembrane PRO polypeptides. The PRO polypeptides are
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
 CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
 CC endometrial bleeding angiogenesis, ischaemia such as coronary
 CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
 CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
 CC diabetes and retinal disorders such as retinitis pigmentosum.
 CC The PRO nucleic acids have applications in molecular biology, including
 CC use as hybridization probes, and in chromosome and gene mapping.

XX Sequence 328 AA;

Query Match 100.0%; Score 70; DB 22; Length 328;

Best Local Similarity 100.0%; Pred. No. 0.00056;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13

|||||

Db 254 DLNKGHLGSEV 266

RESULT 11

AAB53085

ID AAB53085 standard; Protein; 328 AA.

XX

AC AAB53085;

XX

DT 28-FEB-2001 (first entry)

XX

DE Human angiogenesis-associated protein PRO272, SEQ ID NO:113.

XX

KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW myogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal.

XX Homo sapiens.

XX

PN WO200053753-A2.

XX

PD 14-SEP-2000.

XX

XX 05-JAN-2000; 2000WO-US00219.

XX

PR 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 05-OCT-1999; 99WO-US23089.

PR 30-NOV-1999; 99WO-US28313.

PR 30-NOV-1999; 99WO-US28409.

PR 02-DEC-1999; 99WO-US28584.

PR 02-DEC-1999; 99WO-US28565.

XX (GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;

PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;

XX WPI: 2001-090793/10.

DR

DR N-PSDB; AAC97455.

XX New isolated nucleic acid for producing a PRO polypeptide, analyzing

PT genetic disorders and treating cardiovascular, endothelial or

PT angiogenic disorders, such as atherosclerosis, wounds or cancer -

XX

XX Claim 69; Fig 44; 293pp; English.

XX The invention relates to novel human angiogenesis-associated proteins

XX designated PRO proteins (AA853064-B53097), and to nucleic acids encoding

CC PRO proteins. The invention also relates to vectors and host cells

CC comprising a PRO nucleic acid, the recombinant production of a PRO

CC protein, PRO antibodies specific for a PRO protein, fusion proteins

CC comprising a PRO protein, agonists or antagonists of a PRO protein, and

CC compounds which inhibit the expression of a PRO gene. The invention

CC additionally encompasses methods of identifying modulators of PRO

CC expression or activity; diagnosing a cardiovascular, endothelial or

CC angiogenic disorder, or a susceptibility to such a disorder by detecting

CC mutations in a PRO gene, or the expression level of a PRO gene within a

CC particular tissue; treating a cardiovascular, endothelial or angiogenic

CC disorder via the administration of a PRO protein, PRO nucleic acid, or

CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a

CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial

CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the

CC administration of a PRO protein, or an agonist or antagonist thereof.

CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO

CC agonists and PRO antagonists may be used as therapeutic agents to treat

CC cardiovascular, endothelial or angiogenic disorders, such as

CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,

CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,

CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's

CC disease, or stroke. PRO nucleic acids are additionally useful in the

CC recombinant production of PRO proteins, as hybridisation probes to

CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,

CC to map genes encoding PRO proteins, to analyse genetic disorders, and in

CC gene therapy. PRO nucleic acids can also be used to produce transgenic

CC animals useful for the development and screening of potential

CC therapeutic agents. The present sequence represents a PRO protein of the

XX invention.

XX

XX Sequence 328 AA;

XX

XX Query Match 100.0%; Score 70; DB 22; Length 328;

XX Best Local Similarity 100.0%; Pred. No. 0.00056;

XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLNKGDLGSEV 13

Db 254 DLNKGDLGSEV 266

RESULT 12

AAU87402

ID AAU87402 standard; Protein; 343 AA.

XX

XX AC AAU87402;

XX

XX 05-JUN-2002 (first entry)

DT

DE Novel central nervous system protein #312.

XX

XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;

KW hyperproliferative disorder; neoplasm; cardiovascular disorder;

KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;

KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;

KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;

KW adenocarcinoma; reproductive system disorder; testicular feminisation;

KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;

KW respiratory disorder; renal disorder; kidney failure; blood disorder;

KW myocardial infarction; wound healing; cell proliferation; skin aging;

KW food additive; food preservative; gene therapy.

XX

OS Homo sapiens.

XX WO200155318-A2.

PN

XX

PD 02-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US01332.

XX

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.

PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.

PR 22-AUG-2000; 2000US-0226868.

PR 22-AUG-2000; 2000US-0227182.

PR 23-AUG-2000; 2000US-0227009.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0229287.

PR 01-SEP-2000; 2000US-0229343.

PR 01-SEP-2000; 2000US-0229344.

PR 01-SEP-2000; 2000US-0229345.

PR 05-SEP-2000; 2000US-0229509.

PR 05-SEP-2000; 2000US-0229513.

PR 06-SEP-2000; 2000US-0230437.

PR 06-SEP-2000; 2000US-0230438.

PR 08-SEP-2000; 2000US-0231242.

PR 08-SEP-2000; 2000US-0231243.

PR 08-SEP-2000; 2000US-0231244.

PR 08-SEP-2000; 2000US-0231413.

PR 08-SEP-2000; 2000US-0231414.

PR 08-SEP-2000; 2000US-0232080.

PR 08-SEP-2000; 2000US-0232081.

PR 12-SEP-2000; 2000US-0232397.

PR 14-SEP-2000; 2000US-0232398.

PR 14-SEP-2000; 2000US-0232399.

PR 14-SEP-2000; 2000US-0232400.

PR 14-SEP-2000; 2000US-0232401.

PR 14-SEP-2000; 2000US-0233063.

PR 14-SEP-2000; 2000US-0233064.

PR 14-SEP-2000; 2000US-0233065.

PR 21-SEP-2000; 2000US-0234223.

PR 21-SEP-2000; 2000US-0234274.

PR 25-SEP-2000; 2000US-0234997.

PR 25-SEP-2000; 2000US-0234998.

PR 26-SEP-2000; 2000US-0235484.

PR 27-SEP-2000; 2000US-0235834.

PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0241617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA

PI Rosen CA, Barash SC, Ruben SM;
 XX WPI: 2001-581633/65.
 DR N-PSDB; ABR43732.
 XX
 PT New isolated nucleic acid encoding a protein for diagnosing,
 PT preventing, treating or ameliorating medical conditions and used as
 PT food additives or preservatives -
 XX
 PS Claim 9; SEQ ID NO 920; 837pp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule (I) encoding a
 CC novel central nervous system protein. (I) and polypeptides (III) encoded
 CC by (I), are used to treat a medical conditions and in diagnosis of a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angiotrophic lateral sclerosis, infections caused by bacteria, viruses
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
 CC adenocarcinomas and irritable bowel syndrome, reproductive system
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
 CC leukaemia, disorders involving neovascularisation e.g. malignancies,
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
 CC acute kidney failure and blood related disorders e.g. myocardial
 CC infarction. The polypeptides can also be used to aid wound healing and
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 Query Match 100.0%; Score 70; DB 22; Length 343;
 Best Local Similarity 100.0%; Pred. No. 0.00059;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLNKGHLGSEV 13
 Db 269 DLNKGHLGSEV 281
 RESULT 13
 AAM43584
 ID AAM43584 standard; Protein: 343 AA.
 XX
 AC AAM43584;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 262.
 XX
 KW Human: antiarthritic; antirheumatic; antiproliferative; vasotropic;
 KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
 KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
 KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
 KW antiinflammatory; antitumor; cancer; cancer; anticonvulsant; antibacterial;
 KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
 KW cardiovascular disorder; neurological disease; infection; human.
 XX Homo sapiens.
 OS
 XX WO200155308-A2.
 PN
 XX 02-AUG-2001.
 PD
 XX 17-JAN-2001; 2001WO-US01309.
 PF
 XX 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.

CC The invention relates to human polynucleotides (AA163803-AA164012) and
 CC the encoded proteins (AA434497-AA43560) useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. The
 CC genes were isolated from a range of human tissues disclosed in the
 CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
 CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
 CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
 CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
 CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 343 AA;

Query Match 100.0%; Score 70; DB 22; Length 343;
 Best Local Similarity 100.0%; Pred. No. 0.00059;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLGDSV 13
 |||||
 DB 269 DLNKGHLGDSV 281

RESULT 14

AAU19946
 ID AAU19946 standard; Protein; 343 AA.

AC AAU19946;

DT 04-DEC-2001 (first entry)

DE Novel human calcium-binding protein #55.

XX Human; calcium-binding protein; calcium flux; neurological disease;
 KW immune dysfunction; digestive disorder; neoplastic disease;
 KW blood disorder; infectious disease; gene therapy; immunosuppressive;
 KW antithratic; cytosolic; vasotropic; antibacterial; nootropic;
 KW virucide.

XX Homo sapiens.

XX WO200155304-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01302.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

XX 07-JUL-2000; 2000US-0216647.

XX 07-JUL-2000; 2000US-0216880.

XX 11-JUL-2000; 2000US-0217487.

XX 11-JUL-2000; 2000US-0217496.

XX 14-JUL-2000; 2000US-0218290.

XX 26-JUL-2000; 2000US-0220963.

XX 26-JUL-2000; 2000US-0220964.

XX 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.
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 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226688.
 PR 23-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234907.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 13-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
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 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0244674.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.

PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249219.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251368.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465568/50.
N-PSDB; AAS31631.

Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition -

Claim 11; SEQ ID NO 143; 542pp; English.

The present invention relates to the isolation of novel human calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic sequences encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amyotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SCID), digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AAU19892-AAU19969 represent the novel human calcium-binding proteins.

Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 343 AA;

Query Match 100.0%; Score 70; DB 22; Length 343;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13

Db 269 DLNKGHLDGSEV 281

RESULT 15

ABB27587

ID ABB27587 standard; Peptide; 66 AA.

XX

AC ABB27587;

XX

DT 01-FEB-2002 (first entry)

XX

DE Human peptide #238 encoded by breast cell single exon nucleic acid probe.

XX

KW Human; microarray; single exon probe; gene expression; breast;

KW disease; cancer.

XX

OS Homo sapiens.

XX

PN WO200157271-A2.

XX

PD 09-AUG-2001.

XX

PF 30-JAN-2001; 2001WO-US00562.

XX

PR 04-FEB-2000; 2000US-0180312.

PR

PR 26-MAY-2000; 2000US-0207456.

PR

PR 30-JUN-2000; 2000US-0608408.

PR

PR 03-AUG-2000; 2000US-0632366.

PR

PR 21-SEP-2000; 2000US-0234687.

PR

PR 27-SEP-2000; 2000US-0236359.

PR

PR 04-OCT-2000; 2000GB-0024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

DR WPI; 2001-496933/54.

XX

PT New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -

XX

PS Claim 27; SEQ ID NO 10555; 327pp + sequence listing; English.

XX

CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a peptide encoded by a single exon nucleic acid
CC probe of the invention.

CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 66 AA;

Query Match 68.68; Score 48; DB 22; Length 66;
Best Local Similarity 69.28; Pred. No. 0.56;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKDGHLDGSEV 13

Db 27 DLNKDGLDKDEI 39

Search completed: May 14, 2003, 10:42:57
Job time : 5.1173 secs

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GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2003, 10:34:02 ; Search time 103.883 Seconds
(without alignments)
420.726 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 1772
Sequence: 1 MMWRPSVILLLLRRHQAQ.....FVGSQATNYGEDLTRHDEL 328

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	1772	100.0	328	19 AAW80746	Human calcium-bind
2	1772	100.0	328	20 AAY13382	Amino acid sequenc
3	1772	100.0	328	20 AAY00916	Human reticulocalb
4	1772	100.0	328	21 AAB33424	Human PRO272 prote
5	1772	100.0	328	21 AAY53640	A bone marrow secr
6	1772	100.0	328	22 AAU12353	Human PRO272 polyp
7	1772	100.0	328	22 AAG64865	Human calcium bind
8	1772	100.0	328	22 AAB80250	Human PRO272 prote
9	1772	100.0	328	22 AAB53085	Human angiogenesis
10	1764	99.5	343	22 AAU87402	Novel central nerv

11	1764	99.5	343	22 AAW43584	Human polypeptide
12	1764	99.5	343	22 AAU19946	Novel human calciu
13	1761	99.4	328	20 AAW67852	Human secreted pro
14	978	55.2	240	22 AAG75587	Human colon cancer
15	967	54.6	184	20 AAW67906	Human secreted pro
16	956	54.0	311	23 ABP41959	Human ovarian anti
17	944	53.3	331	22 AAG64866	Human reticulocalb
18	944	53.3	331	22 AAO17363	Human reticulocalb
19	938	52.9	325	22 AAG64867	Murine reticulocal
20	857.5	48.4	315	22 AAB94090	Human reticulocal
21	857.5	48.4	315	23 AAU84387	Human protein sequ
22	842.5	47.5	315	19 AAW37865	Novel human secret
23	842.5	47.5	315	20 AAY00917	Human protein comp
24	842.5	47.5	315	20 AAW67886	Human reticulocalb
25	833.5	47.0	315	22 AAW93808	Human secreted pro
26	482	27.2	96	20 AAY11533	Human polypeptide,
27	457	25.8	342	22 ABB64246	Human 5' EST secre
28	456.5	25.8	317	18 AAW21949	Drosophila melanog
29	456.5	25.8	349	23 ABP41860	E6-binding protein
30	449.5	25.4	317	23 AAG65817	Human ovarian anti
31	448.5	25.3	192	22 ABB57787	Human reticulocalb
32	362.5	20.5	219	17 AAR77660	Drosophila melanog
33	347	19.6	119	22 AAW93520	HPV E6-binding pro
34	266.5	15.0	362	18 AAW12373	Human polypeptide,
35	260.5	14.7	361	18 AAW12372	Human stromal cell
36	230.5	13.0	259	22 AAB93731	Mouse stromal cell
37	220	12.4	450	18 AAW12375	Human protein sequ
38	205	11.6	94	20 AAY12347	Human stromal cell
39	196	11.1	66	22 ABB27587	Human 5' EST secre
40	196	11.1	66	22 ABB32751	Human peptide #238
41	196	11.1	66	22 ABB18233	Protein #257 encod
42	196	11.1	66	22 AAW53562	Human brain expres
43	196	11.1	66	22 AAW65945	Human bone marrow
44	196	11.1	66	22 AAW13812	Peptide #246 encod
45	196	11.1	66	22 AAW26213	Peptide #250 encod

ALIGNMENTS

RESULT 1
AAW80746
ID AAW80746 standard; Protein; 328 AA.
AC AAW80746;
XX
XX
XX 15-DEC-1998 (first entry)
DT
DE Human calcium-binding protein.
XX
XX Human; calcium-binding protein; reticulocalbin; sickle cell anaemia;
KW HCBP; beta thalassaemia; cell proliferation; cancer; adenocarcinoma;
KW leukemia; lymphoma; melanoma; sarcoma.
XX
OS Homo sapiens.
XX
XX WO9844114-A1.
PN
XX
PD 08-OCT-1998.
XX
XX 30-MAR-1998; 98WO-US06233.
PF
XX 31-MAR-1997; 97US-0828242.
PR
XX (INCY-) INCYTE PHARM INC.
XX
XX Goli SK, Hillman JL;
XX
XX WPI; 1998-542704/46.
DR N-PSDB; AAW57600.
XX
XX A new human calcium binding protein - useful for treating or
PT preventing disorders associated with the expression of HCBP

XX Claim 1; Page 42-43; 60pp; English.
XX
CC The present sequence is a new human calcium binding protein (HCBP).
CC A pharmaceutical composition which includes the HCBP protein is claimed
CC and can be added directly to cells in vivo to promote regeneration or
CC differentiation of cells. HCBP can also be added to cells, cell lines,
CC tissue or organ culture to stimulate cell proliferation for heterologous
CC and autologous transplantation. The cells can be selected for their
CC ability to inhibit development of an infection or to correct a genetic
CC defect such as sickle cell anemia, beta thalassemia. An antagonist of
CC HCBP can be administered to a subject to treat or prevent a disorder
CC associated with cell proliferation e.g. many cancers including
CC adenocarcinoma, leukemia, lymphoma, melanoma, sarcoma and particularly
CC cancers of bladder, bone, brain, heart, kidney, liver. Antibodies
CC specific for HCBP may be used directly as an antagonist or indirectly as
CC a targeting or delivery mechanism for delivering pharmaceutical agents
CC to cell or tissue which express protein HCBP. A method is claimed for
CC treating or preventing a disorder associated with cell proliferation
CC which involves adding pharmaceutical composition of antagonist of HCBP.
XX
SQ Sequence 328 AA;

Query Match 100.0%; Score 1772; DB 19; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.7e-155;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMWRPSVLLLLLRHGAQCKPSDAGPHGGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
DB 1 MMWRPSVLLLLLRHGAQCKPSDAGPHGGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
QY 61 GREVAKFEFDQLTPESQARLGRIYDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
DB 61 GREVAKFEFDQLTPESQARLGRIYDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 AWDYTDYDRGVRGWEELRNATYGHYAPGEEFHDVEADYKMKLARDERFRVADQDGD 180
DB 121 AWDYTDYDRGVRGWEELRNATYGHYAPGEEFHDVEADYKMKLARDERFRVADQDGD 180
QY 181 SMATREELTAFLHPPEPHMDIVIAETLEDLRNKGQYQVVEYIADLYSAEPGEPEPA 240
DB 181 SMATREELTAFLHPPEPHMDIVIAETLEDLRNKGQYQVVEYIADLYSAEPGEPEPA 240
QY 241 WVQTERQQRFDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTRDKDRLSKA 300
DB 241 WVQTERQQRFDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTRDKDRLSKA 300
QY 301 EILGNWNMFVGSQATNYGDELTRHDEL 328
DB 301 EILGNWNMFVGSQATNYGDELTRHDEL 328

RESULT 2
AAY13382
ID AAY13382 standard; Protein; 328 AA.
XX
XX AAY13382;
XX
XX 25-JUN-1999 (first entry)
XX
XX Amino acid sequence of protein PRO272.
XX
XX Secreted protein; transmembrane protein; human; enterocolitis;
XX Zollinger-Ellison syndrome; gastrointestinal ulceration;
XX congenital microvillus atrophy; skin disease; cell growth;
XX abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
XX Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
XX fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
XX anti-thrombotic; wound healing; tissue repair.
XX
XX Homo sapiens.
XX
PN W09914328-A2.

XX 25-MAR-1999.
PD 98WO-US19330.
XX
XX 16-SEP-1998;
PF 97US-0066840.
XX 25-NOV-1997;
PR 97US-0059113.
PR 17-SEP-1997;
PR 97US-0059115.
PR 17-SEP-1997;
PR 97US-0059117.
PR 17-SEP-1997;
PR 97US-0059119.
PR 17-SEP-1997;
PR 97US-0059121.
PR 17-SEP-1997;
PR 97US-0059122.
PR 17-SEP-1997;
PR 97US-0059184.
PR 18-SEP-1997;
PR 97US-0059263.
PR 15-OCT-1997;
PR 97US-0062125.
PR 17-OCT-1997;
PR 97US-0062285.
PR 17-OCT-1997;
PR 97US-0062287.
PR 21-OCT-1997;
PR 97US-0063486.
PR 24-OCT-1997;
PR 97US-0062814.
PR 24-OCT-1997;
PR 97US-0062816.
PR 24-OCT-1997;
PR 97US-0063045.
PR 24-OCT-1997;
PR 97US-0063120.
PR 24-OCT-1997;
PR 97US-0063121.
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PR 97US-0063127.
PR 24-OCT-1997;
PR 97US-0063128.
PR 27-OCT-1997;
PR 97US-0063329.
PR 27-OCT-1997;
PR 97US-0063327.
PR 28-OCT-1997;
PR 97US-0063541.
PR 28-OCT-1997;
PR 97US-0063542.
PR 28-OCT-1997;
PR 97US-0063544.
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PR 97US-0063549.
PR 28-OCT-1997;
PR 97US-0063550.
PR 28-OCT-1997;
PR 97US-0063564.
PR 29-OCT-1997;
PR 97US-0063435.
PR 29-OCT-1997;
PR 97US-0063704.
PR 29-OCT-1997;
PR 97US-0063732.
PR 29-OCT-1997;
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PR 29-OCT-1997;
PR 97US-0063734.
PR 29-OCT-1997;
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PR 29-OCT-1997;
PR 97US-0063735.
PR 31-OCT-1997;
PR 97US-0063870.
PR 31-OCT-1997;
PR 97US-0064103.
PR 03-NOV-1997;
PR 97US-0064248.
PR 07-NOV-1997;
PR 97US-0064809.
PR 12-NOV-1997;
PR 97US-0065186.
PR 17-NOV-1997;
PR 97US-0065846.
PR 18-NOV-1997;
PR 97US-0065693.
PR 21-NOV-1997;
PR 97US-0066120.
PR 21-NOV-1997;
PR 97US-0066364.
PR 24-NOV-1997;
PR 97US-0066772.
PR 24-NOV-1997;
PR 97US-0066466.
PR 24-NOV-1997;
PR 97US-0066770.
PR 24-NOV-1997;
PR 97US-0066511.
PR 24-NOV-1997;
PR 97US-0066453.

(GETH) GENENTECH INC.

Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;

WPI; 1999-229533/19.

N-PSDB; AAX52253.

New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration

Claim 12; Fig 80; 320pp; English.

AAY13344-403 represent secreted and transmembrane human proteins.
The cDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders

associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as a target for anti-tumor drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.

Sequence 328 AA;

Query Match 100.0%; Score 1772; DB 20; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.7e-155;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLLRHGAQGRVHQAAPLSDAPHDHAGNFGYDHEAFL 60
DB 1 MMWRPSVLLLLLLLRHGAQGRVHQAAPLSDAPHDHAGNFGYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRVDRMDRAGDGDGWSLAELRAWTQORHIRDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRVDRMDRAGDGDGWSLAELRAWTQORHIRDSVSA 120
QY 121 AWDYTDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
DB 121 AWDYTDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAFLHPEEPFPHMRDVIATETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPFPHMRDVIATETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WVOTERQQRFRDLNKGHLDSGEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
DB 241 WVOTERQQRFRDLNKGHLDSGEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNMNFVGSQATNYGEDLTRHDEL 328
DB 301 EILGNMNFVGSQATNYGEDLTRHDEL 328

RESULT 3
AAY00916

ID AAY00916 standard; Protein; 328 AA.

XX AC AAY00916;

XX DT 28-MAY-1999 (first entry)

XX DE Human reticulocalbin gamma protein sequence.

XX KW Human; reticulocalbin gamma; RCNdelta; reticulocalbin delta; RCNdelta; development disorder; neoplastic disorder; immunological disorder; infection.

XX OS Homo sapiens.

XX PN WO9907849-A2.

XX PD 18-FEB-1999.

XX PF 05-AUG-1998; 98WO-US16259.

XX PR 08-AUG-1997; 97US-0910927.

XX PA (INCY-) INCYTE PHARM INC.

XX PI

XX DR

XX DR

XX PT

XX PT

XX PS

XX CC

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Bandman O, Corley NC, Hillman JL, Lal P, Shah P;

WPI: 1999-180492/15.

N-PSDB; AAX27229.

New human reticulocalbin isoforms - useful to diagnose, prevent, and treat infectious, developmental, neoplastic, and immunological disorders

Claim 1; Fig 1; 82pp; English.

This sequence is the human reticulocalbin gamma (RCNgamma) of the invention. RCNgamma and RCNdelta are used to treat an infectious or developmental disorder, and antagonists of them are used to treat a neoplastic or immunological disorder. Infectious disorders include e.g. pneumonia, lymphocytic choriomeningitis, Hantavirus, chronic bronchitis, hepatitis, herpesviruses, yellow fever, influenza, cancer, measles, mumps, rhinovirus, poliovirus, coxsackie-virus, smallpox, Colorado tick fever, HIV, rabies, gastroenteritis, and rubella, encephalitis, and bacterial, fungal, parasitic, protozoal, or helminthic infections. Development disorders include e.g. renal tubular acidosis, anaemia, Cushing's syndrome, achondroplastic dwarfism, epilepsy, gonadal dysgenesis, hereditary neuropathies such as Charcot-Marie-Tooth disease, and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders, congenital glaucoma, cataract, or sensorineural hearing loss. Neoplastic disorders include e.g. adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma and teratocarcinoma. Overexpression of reticulocalbin mRNA has been associated with increased matrix invasive properties of three human breast cancer lines.

Sequence 328 AA;

Query Match 100.0%; Score 1772; DB 20; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.7e-155;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLLRHGAQGRVHQAAPLSDAPHDHAGNFGYDHEAFL 60

DB 1 MMWRPSVLLLLLLLRHGAQGRVHQAAPLSDAPHDHAGNFGYDHEAFL 60

QY 61 GREVAKEFDQLTPEESQARLGRVDRMDRAGDGDGWSLAELRAWTQORHIRDSVSA 120

DB 61 GREVAKEFDQLTPEESQARLGRVDRMDRAGDGDGWSLAELRAWTQORHIRDSVSA 120

QY 121 AWDYTDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180

DB 121 AWDYTDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180

QY 181 SMATREELTAFLHPEEPFPHMRDVIATETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240

DB 181 SMATREELTAFLHPEEPFPHMRDVIATETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240

QY 241 WVOTERQQRFRDLNKGHLDSGEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300

DB 241 WVOTERQQRFRDLNKGHLDSGEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300

QY 301 EILGNMNFVGSQATNYGEDLTRHDEL 328

DB 301 EILGNMNFVGSQATNYGEDLTRHDEL 328

RESULT 4

AAB33424

ID AAB33424 standard; Protein; 328 AA.

XX AC AAB33424;

XX DT 29-JAN-2001 (first entry)

XX DE Human PRO272 protein UNQ239 SEQ ID NO:51.

XX

KW	Human; immune related disease; diagnosis; antiinflammatory; cardiant;	PT	immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
KW	dermatological; antiarthritic; antirheumatic; immunosuppressive;	PT	arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
KW	haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;	XX	
KW	antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;	XX	Claim 33; Fig 22; 309pp; English.
KW	asthmatic; systemic lupus erythematosus; rheumatoid arthritis;	XX	
KW	osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;	CC	The present invention describes sixty four human PRO proteins which can
KW	idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;	CC	be used in the treatment of immune related diseases. The human PRO
KW	systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;	CC	proteins, anti-PRO antibodies, agonists and antagonists are useful for
KW	autoimmune thrombocytopenia; immune-mediated renal disease;	CC	treating and diagnosing immune related disorders. The disorders are
KW	demylinating disease; hepatobiliary disease; Whipple's disease;	CC	selected from systemic lupus erythematosus, rheumatoid arthritis,
KW	inflammatory bowel disease; gluten-sensitive enteropathy;	CC	osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
KW	autoimmune disease; immune-mediated skin disease; allergic disease;	CC	systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
KW	immunological disease; transplantation associated disease;	CC	syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
KW	graft rejection; graft-versus-host-disease.	CC	anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
XX		CC	immune-mediated renal disease, demyelinating diseases, inflammatory
OS	Homo sapiens.	CC	and peripheral nervous systems, hepatobiliary diseases, inflammatory
XX		CC	bowel disease, gluten-sensitive enteropathy and Whipple's disease,
XX		CC	autoimmune or immune-mediated skin diseases, allergic diseases,
PN	WO200053758-A2.	CC	immunological diseases of the lung, and transplantation associated
XX		CC	diseases including graft rejection and graft-versus-host-disease.
PD	14-SEP-2000.	CC	AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
XX		CC	in the isolation of human PRO sequences. AAC58579 to AAC58642 and
XX	02-MAR-2000; 2000WO-US05841.	CC	AAB33414 to AAB33477 represent human PRO polynucleotide and protein
XX		CC	sequences given in the exemplification of the present invention.
PR	08-MAR-1999; 99WO-US05028.	XX	Sequence 328 AA;
PR	10-MAR-1999; 99US-0123618.		Query Match 100.0%; Score 1772; DB 21; Length 328;
PR	12-MAR-1999; 99US-0123957.		Best Local Similarity 100.0%; Pred. No. 1.7e-155;
PR	23-MAR-1999; 99US-0125775.		Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR	12-APR-1999; 99US-0128849.		
PR	20-APR-1999; 99WO-US08615.	QY	1 MMWRPSVLLLLLRHGAQGKPSDPAGHGQGRVHOAAPLSDAPHDHAGNFQYDHEAFL 60
PR	28-APR-1999; 99US-0131445.	Db	1 MMWRPSVLLLLLRHGAQGKPSDPAGHGQGRVHOAAPLSDAPHDHAGNFQYDHEAFL 60.
PR	04-MAY-1999; 99US-0132371.	QY	61 GREVAKFDDLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWTIAHTQORHIRDSVA 120
PR	14-MAY-1999; 99US-0134287.	Db	61 GREVAKFDDLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWTIAHTQORHIRDSVA 120
PR	02-JUN-1999; 99WO-US12252.	QY	121 AWDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETTKMLARDERRFRVADQGD 180
PR	23-JUN-1999; 99US-0141037.	Db	121 AWDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETTKMLARDERRFRVADQGD 180
PR	20-JUL-1999; 99US-0144758.	QY	181 SMATREELTAFLHPPEEPHMRDIVIAETLEDLRNKDGYQVEEYIADLYSAEPEEPA 240
PR	26-JUL-1999; 99US-0145698.	Db	181 SMATREELTAFLHPPEEPHMRDIVIAETLEDLRNKDGYQVEEYIADLYSAEPEEPA 240
PR	28-JUL-1999; 99US-0146222.	QY	241 WVQTERQQFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTRDKDGRLSKA 300
PR	01-SEP-1999; 99WO-US20111.	Db	241 WVQTERQQFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTRDKDGRLSKA 300
PR	08-SEP-1999; 99WO-US20594.	QY	301 EILGNWNMFVGSQATNYGEDLTRHDEL 328
PR	13-SEP-1999; 99WO-US20944.	Db	301 EILGNWNMFVGSQATNYGEDLTRHDEL 328
PR	15-SEP-1999; 99WO-US21090.		RESULT 5
PR	15-SEP-1999; 99WO-US21547.		AA53640
PR	05-OCT-1999; 99US-0162508.	ID	AA53640 standard; Protein: 328 AA.
PR	29-OCT-1999; 99US-0162509.	XX	
PR	29-NOV-1999; 99WO-US28214.	XX	AA53640;
PR	30-NOV-1999; 99WO-US28313.	XX	
PR	30-NOV-1999; 99WO-US28409.	DT	22-FEB-2000 (first entry)
PR	01-DEC-1999; 99WO-US28301.	XX	
PR	01-DEC-1999; 99WO-US28634.	DE	A bone marrow secreted protein designated BMS37.
PR	02-DEC-1999; 99WO-US28551.	XX	
PR	02-DEC-1999; 99WO-US28564.	XX	Bone marrow secreted protein; bone marrow stromal cell; cytokine;
PR	02-DEC-1999; 99WO-US28565.	XX	cell proliferation; cell differentiation; hematopoiesis; anaemia;
PR	16-DEC-1999; 99WO-US30095.	KW	myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
PR	30-DEC-1999; 99WO-US31274.	KW	erythroid progenitor cell; colony stimulating factor; granulocyte;
PR	05-JAN-2000; 2000WO-US00219.	KW	monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
PR	06-JAN-2000; 2000WO-US00277.	KW	platelet disorder; thrombocytopenia; hematopoietic stem cell;
PR	06-JAN-2000; 2000WO-US00376.	XX	stem cell disorder; aplastic anaemia; bone differentiation;
PR	11-FEB-2000; 2000WO-US03565.	DR	
PR	18-FEB-2000; 2000WO-US04341.	DR	WPI: 2000-572271/53.
PR	18-FEB-2000; 2000WO-US04342.	XX	N-PSDB; AAC58589.
PR	22-FEB-2000; 2000WO-US04414.	XX	
XX		PA	(GETH) GENENTECH INC.
PI	Ashtkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;	PI	
PI	Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;	PI	
PI	Stewart TA, Tumas D, Watanabe CK, Wood WL, Yan M;	XX	
XX		XX	
DR	WPI: 2000-572271/53.	DR	
XX	N-PSDB; AAC58589.	XX	
XX		XX	Sixty four PRO polypeptides, useful in the diagnosis and treatment of

DR WPI; 2001-408281/43.
DR N-PSDB; AAS21425.
XX Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical
XX
XX Claim 12; Fig 364; 813pp; English.
XX
XX AAU12172-AAU12446 represent novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIa. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
XX Sequence 328 AA;
SQ
Query Match 100.0%; Score 1772; DB 22; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.7e-155;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMWRPVLVLLLLLRHGAQKPSDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
DB 1 MMWRPVLVLLLLLRHGAQKPSDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADTYKKMLARDERRFRVADQDGD 180
DB 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADTYKKMLARDERRFRVADQDGD 180
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WYQTERQOFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
DB 241 WYQTERQOFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNMNMVFGSQATNYGDLTRHDEL 328
DB 301 EILGNMNMVFGSQATNYGDLTRHDEL 328
RESULT 7
AAG64865
ID AAG64865 standard; protein; 328 AA.
XX
AC AAG64865;
XX
XX 21-SEP-2001 (first entry)
DT Human calcium binding protein.
DE Human; calcium binding protein; HCBP; cell proliferation disorder;
XX
KW

KW cancer.
XX
XX Homo sapiens.
XX
PN US2001012831-A1.
XX
PD 09-AUG-2001.
XX
PF 23-JAN-2001; 2001US-0768840.
XX
PR 21-MAR-1997; 97US-0828212.
PR 07-DEC-1998; 98US-0206499.
XX
PA (INCY-) INCYTE PHARM INC.
XX
XX Hillman JL, Goli SK;
XX WPI; 2001-464391/50.
DR N-PSDB; AAH48279.
XX
XX Human calcium-binding protein, useful in the diagnosis, prevention, and
PT treatment of disorders associated with cell proliferation, e.g.
PT adenocarcinoma, leukemia, lymphoma, melanoma, sarcoma, or
PT teratocarcinoma.
XX
PS Claim 1; Fig 1; 30pp; English.
XX
XX The present invention provides the protein and coding sequences of human
CC calcium binding protein (HCBP). The sequences can be used in the
CC diagnosis, prevention and treatment of cell proliferation disorders, such
CC as cancer. The present sequence is the protein of the invention.
XX
XX Sequence 328 AA;
SQ
Query Match 100.0%; Score 1772; DB 22; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.7e-155;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMWRPVLVLLLLLRHGAQKPSDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
DB 1 MMWRPVLVLLLLLRHGAQKPSDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADTYKKMLARDERRFRVADQDGD 180
DB 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADTYKKMLARDERRFRVADQDGD 180
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WYQTERQOFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
DB 241 WYQTERQOFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNMNMVFGSQATNYGDLTRHDEL 328
DB 301 EILGNMNMVFGSQATNYGDLTRHDEL 328
RESULT 8
AAB80250
ID AAB80250 standard; protein; 328 AA.
XX
AC AAB80250;
XX
XX 24-APR-2001 (first entry)
DT Human PRO272 protein.
DE
XX
XX

Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory; antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer; antiarthritic; antinfertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder; ischaemia; inflammation.

Human sapiens.

WO200104311-A1.

18-JAN-2001.

22-FEB-2000; 2000WO-US04414.

07-JUL-1999; 99US-0143048.

26-JUL-1999; 99US-0145698.

28-JUL-1999; 99US-0146222.

08-SEP-1999; 99WO-US20594.

13-SEP-1999; 99WO-US20594.

15-SEP-1999; 99WO-US21090.

15-SEP-1999; 99WO-US21547.

05-OCT-1999; 99WO-US23089.

29-NOV-1999; 99WO-US28214.

30-NOV-1999; 99WO-US28313.

16-DEC-1999; 99WO-US30095.

20-DEC-1999; 99WO-US30911.

20-DEC-1999; 99WO-US30999.

05-JAN-2000; 99WO-US00219.

(GETH) GENENTECH INC.

Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Flivaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kijavini LJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI: 2001-081051/09.

N-PSDB; AAF72411.

Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's disease).

Claim 1: Fig 80; 393pp; English.

The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosa.

The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.

Sequence 328 AA:

Query Match
Best Local Similarity 100.0%; Score 1772; DB 22; Length 328;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPVLVLLLLRHGAGKPSDPAGPHGGRVHQARPLSDAPDHDAHGNFYDHEAFL 60
|||||

Db 1 MMWRPVLVLLLLRHGAGKPSDPAGPHGGRVHQARPLSDAPDHDAHGNFYDHEAFL 60
|||||

QY 61 GREVAKFDQLTPEESQARLGRIVDRMDRAGDGGVSLAEALRAWIAHTQORHIRDSVSA 120
|||||

Db 61 GREVAKFDQLTPEESQARLGRIVDRMDRAGDGGVSLAEALRAWIAHTQORHIRDSVSA 120

QY 121 AWDTYDTRDRGRVGEELRNATYGHVAPGEEFHVDVEDAETYYKMLARDERRFRVADQGD 180
|||||

Db 121 AWDTYDTRDRGRVGEELRNATYGHVAPGEEFHVDVEDAETYYKMLARDERRFRVADQGD 180
|||||

QY 181 SMATREELTAFLHPEEFPHMRDIIAETLEDLDRNKDGVQVVEYIADLYSAEPGEEPA 240
|||||

Db 181 SMATREELTAFLHPEEFPHMRDIIAETLEDLDRNKDGVQVVEYIADLYSAEPGEEPA 240
|||||

QY 241 WYOTERQOQFRDLNKNKDLGSGSEVGHVWLPAPQDPLVEANHLHESDTRKDGRLSKA 300
|||||

Db 241 WYOTERQOQFRDLNKNKDLGSGSEVGHVWLPAPQDPLVEANHLHESDTRKDGRLSKA 300
|||||

QY 301 EILGNMNFVGSQATNYGEDLTRHDEL 328
|||||

Db 301 EILGNMNFVGSQATNYGEDLTRHDEL 328
|||||

RESULT 9

AAB53085

ID AAB53085 standard; Protein; 328 AA.

XX

AC AAB53085;

XX

DT 28-FEB-2001 (first entry)

XX

DE Human angiogenesis-associated protein PRO272, SEQ ID NO:113.

XX

KW Human; angiogenesis-associated protein; PRO; endothelial cell growth; cardiac hypertrophy; cardiovascular disorder; endothelial disorder; angiocardial infarction; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer; Alzheimer's disease; Huntington's disease; stroke; drug screening; gene therapy; transgenic animal.

XX

OS Homo sapiens.

XX

PN WO2000053753-A2.

XX

PD 14-SEP-2000.

XX

PF 05-JAN-2000; 2000WO-US00219.

XX

ER 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 05-OCT-1999; 99WO-US23089.

PR 30-NOV-1999; 99WO-US28313.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

XX

PA (GETH) GENENTECH INC.

XX

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Matsters SA;

PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;

XX WPI: 2001-090793/10.

DR N-PSDB; AAC97455.

XX

PT New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or

05-JUN-2002 (first entry)
Novel central nervous system protein #312.

Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cerebrovascular disorder; ischaemia; angiodenesis; cardiac arrest; Alzheimer's disease; AIDS; ocular disorder; nervous system disorder; dysphagia; gastrointestinal disorder; acquired immunodeficiency virus; reproductive system disorder; testicular feminisation; adenocarcinoma; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy.

Homo sapiens.	
W0200155318-A2.	
02-AUG-2001.	
17-JAN-2001; 2001W0-US01332.	
31-JAN-2000; 2000US-0179065.	
04-FEB-2000; 2000US-0180628.	
24-FEB-2000; 2000US-0184664.	
02-MAR-2000; 2000US-0186350.	
16-MAR-2000; 2000US-0189874.	
17-MAR-2000; 2000US-0190076.	
18-APR-2000; 2000US-0198123.	
19-MAY-2000; 2000US-0205515.	
07-JUN-2000; 2000US-0209467.	
28-JUN-2000; 2000US-0214886.	
30-JUN-2000; 2000US-0215135.	
07-JUL-2000; 2000US-0216647.	
07-JUL-2000; 2000US-0216680.	
11-JUL-2000; 2000US-0217487.	
11-JUL-2000; 2000US-0217496.	
14-JUL-2000; 2000US-0218290.	
26-JUL-2000; 2000US-0220363.	
26-JUL-2000; 2000US-0220364.	
14-AUG-2000; 2000US-0224518.	
14-AUG-2000; 2000US-0224519.	
14-AUG-2000; 2000US-0225213.	
14-AUG-2000; 2000US-0225214.	
14-AUG-2000; 2000US-0225266.	
14-AUG-2000; 2000US-0225367.	
14-AUG-2000; 2000US-0225368.	
14-AUG-2000; 2000US-0225270.	
14-AUG-2000; 2000US-0225447.	
14-AUG-2000; 2000US-0225757.	
14-AUG-2000; 2000US-0225758.	
14-AUG-2000; 2000US-0225759.	
14-AUG-2000; 2000US-0226079.	
18-AUG-2000; 2000US-0226681.	
22-AUG-2000; 2000US-0226686.	
22-AUG-2000; 2000US-0227182.	
23-AUG-2000; 2000US-0227009.	
30-AUG-2000; 2000US-0228924.	
01-SEP-2000; 2000US-0229287.	
01-SEP-2000; 2000US-0229343.	
01-SEP-2000; 2000US-0229344.	
01-SEP-2000; 2000US-0229345.	
05-SEP-2000; 2000US-0229509.	
05-SEP-2000; 2000US-0229513.	
06-SEP-2000; 2000US-0230437.	
06-SEP-2000; 2000US-0230438.	
08-SEP-2000; 2000US-0231242.	
08-SEP-2000; 2000US-0231243.	
08-SEP-2000; 2000US-0231244.	
08-SEP-2000; 2000US-0231414.	
08-SEP-2000; 2000US-0232080.	

RESULT 10
AAU87402
ID AAU87
XX
AC AAU87
XX

Matches	327;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	MMWRPSVLLLLLLL	RHCAQCKSP	DACPHGCGR	VHQAPLSD	ADPHDDAHG	NFQYDHAFL	60	
Db	16	MMWRPSVLLLLLLL	RHCAQCKSP	DACPHGCGR	VHQAPLSD	ADPHDDAHG	NFQYDHAFL	75	
QY	61	GREVAKFDDQLT	PESQARLGR	IVDRMDR	AGDGGW	SLAELRA	WIAHTQQR	120	
Db	76	GREVAKFDDQLT	PESQARLGR	IVDRMDR	AGDGGW	SLAELRA	WIAHTQQR	135	
QY	121	AWDTYDTRDGR	GWEELRNAT	YGHPGEEF	HDEDAETY	KKMLARDE	RRFVADODGD	180	
Db	136	AWDTYDTRDGR	GWEELRNAT	YGHPGEEF	HDEDAETY	KKMLARDE	RRFVADODGD	195	
QY	181	SMATREELTAFL	PEEPHMRD	IVIAETLED	LDRNKDGY	VQVEEY	IADLYSA	240	
Db	196	SMATREELTAFL	PEEPHMRD	IVIAETLED	LDRNKDGY	VQVEEY	IADLYSA	255	
QY	241	WVQTERQQP	DRFDRLN	KDGHLD	SGVGHW	YLPAPQD	PLVEANHLLH	300	

Tue May 20 14:43:27 2003

us-09-768-840-1.rag

Db	256	WVQTERQQFWDFRDLNKGDLGSEVGHVWLP	PAQDQPLVEANHLLHESDTDKDGLSKA	315
QY	301	EILGNWMMFVGSQATNYGEDLTRHDEL	328	
Db	316	EILGNWMMFVGSQATNYGEDLTRHDEL	343	
RESULT 11				
AA443584				
ID	AA443584 standard; Protein; 343 AA.			
XX	AA443584;			
DT	22-OCT-2001 (first entry)			
XX	Human polypeptide SEQ ID NO 262.			
DE	XX			
XX	Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;			
KW	cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;			
KW	fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;			
KW	neuroprotective; antiallergic; hepatotropic; antidiabetic;			
KW	antiinflammatory; antitumor; antitumor; antitumor; antitumor;			
KW	antiparasitic; cardiac; gene therapy; cancer; immune disorder;			
KW	cardiovascular disorder; neurological disease; infection; human.			
OS	Homo sapiens.			
XX	WO200155308-A2.			
PN	02-AUG-2001.			
PD	17-JAN-2001; 2001WO-US01309.			
XX	31-JAN-2000; 2000US-0179065.			
PR	04-FEB-2000; 2000US-0180628.			
PR	24-FEB-2000; 2000US-0184664.			
PR	02-MAR-2000; 2000US-0186350.			
PR	16-MAR-2000; 2000US-0189874.			
PR	17-MAR-2000; 2000US-0190076.			
PR	18-APR-2000; 2000US-0198123.			
PR	19-MAY-2000; 2000US-0205515.			
PR	07-JUN-2000; 2000US-0209467.			
PR	30-JUN-2000; 2000US-0215135.			
PR	07-JUL-2000; 2000US-0216647.			
PR	07-JUL-2000; 2000US-0216880.			
PR	11-JUL-2000; 2000US-0217487.			
PR	11-JUL-2000; 2000US-0217496.			
PR	14-JUL-2000; 2000US-0218290.			
PR	26-JUL-2000; 2000US-0220963.			
PR	14-AUG-2000; 2000US-0220964.			
PR	14-AUG-2000; 2000US-0224518.			
PR	14-AUG-2000; 2000US-0224519.			
PR	14-AUG-2000; 2000US-0225213.			
PR	14-AUG-2000; 2000US-0225214.			
PR	14-AUG-2000; 2000US-0225266.			
PR	14-AUG-2000; 2000US-0225267.			
PR	14-AUG-2000; 2000US-0225268.			
PR	14-AUG-2000; 2000US-0225270.			
PR	14-AUG-2000; 2000US-0225447.			
PR	14-AUG-2000; 2000US-0225757.			
PR	14-AUG-2000; 2000US-0225758.			
PR	14-AUG-2000; 2000US-0225759.			
PR	18-AUG-2000; 2000US-0226279.			
PR	22-AUG-2000; 2000US-0226681.			
PR	22-AUG-2000; 2000US-0226688.			
PR	22-AUG-2000; 2000US-0227182.			
PR	23-AUG-2000; 2000US-0227009.			
PR	30-AUG-2000; 2000US-0228924.			
PR	01-SEP-2000; 2000US-0229287.			
PR	01-SEP-2000; 2000US-0229343.			
PR	01-SEP-2000; 2000US-0229344.			
PR	01-SEP-2000; 2000US-0229345.			
PR	05-SEP-2000; 2000US-0229509.			
PR	05-SEP-2000; 2000US-0229513.			
PR	06-SEP-2000; 2000US-0230437.			
PR	06-SEP-2000; 2000US-0230438.			
PR	08-SEP-2000; 2000US-0231242.			
PR	08-SEP-2000; 2000US-0231243.			
PR	08-SEP-2000; 2000US-0231244.			
PR	08-SEP-2000; 2000US-0231413.			
PR	08-SEP-2000; 2000US-0231414.			
PR	08-SEP-2000; 2000US-0232080.			
PR	08-SEP-2000; 2000US-0232081.			
PR	12-SEP-2000; 2000US-0231968.			
PR	14-SEP-2000; 2000US-0232397.			
PR	14-SEP-2000; 2000US-0232398.			
PR	14-SEP-2000; 2000US-0232399.			
PR	14-SEP-2000; 2000US-0232400.			
PR	14-SEP-2000; 2000US-0232401.			
PR	14-SEP-2000; 2000US-0233063.			
PR	14-SEP-2000; 2000US-0233064.			
PR	14-SEP-2000; 2000US-0233065.			
PR	21-SEP-2000; 2000US-0234223.			
PR	21-SEP-2000; 2000US-0234274.			
PR	25-SEP-2000; 2000US-0234997.			
PR	25-SEP-2000; 2000US-0234998.			
PR	26-SEP-2000; 2000US-0235484.			
PR	27-SEP-2000; 2000US-0235834.			
PR	27-SEP-2000; 2000US-0235836.			
PR	29-SEP-2000; 2000US-0236327.			
PR	29-SEP-2000; 2000US-0236367.			
PR	29-SEP-2000; 2000US-0236368.			
PR	29-SEP-2000; 2000US-0236369.			
PR	29-SEP-2000; 2000US-0236370.			
PR	02-OCT-2000; 2000US-0236802.			
PR	02-OCT-2000; 2000US-0237037.			
PR	02-OCT-2000; 2000US-0237038.			
PR	02-OCT-2000; 2000US-0237039.			
PR	02-OCT-2000; 2000US-0237040.			
PR	13-OCT-2000; 2000US-0239935.			
PR	13-OCT-2000; 2000US-0239937.			
PR	20-OCT-2000; 2000US-0240960.			
PR	20-OCT-2000; 2000US-0241221.			
PR	20-OCT-2000; 2000US-0241785.			
PR	20-OCT-2000; 2000US-0241786.			
PR	20-OCT-2000; 2000US-0241787.			
PR	20-OCT-2000; 2000US-0241808.			
PR	20-OCT-2000; 2000US-0241809.			
PR	20-OCT-2000; 2000US-0241826.			
PR	01-NOV-2000; 2000US-0244617.			
PR	08-NOV-2000; 2000US-0246474.			
PR	08-NOV-2000; 2000US-0246475.			
PR	08-NOV-2000; 2000US-0246476.			
PR	08-NOV-2000; 2000US-0246477.			
PR	08-NOV-2000; 2000US-0246478.			
PR	08-NOV-2000; 2000US-0246523.			
PR	08-NOV-2000; 2000US-0246524.			
PR	08-NOV-2000; 2000US-0246525.			
PR	08-NOV-2000; 2000US-0246526.			
PR	08-NOV-2000; 2000US-0246527.			
PR	08-NOV-2000; 2000US-0246528.			
PR	08-NOV-2000; 2000US-0246532.			
PR	08-NOV-2000; 2000US-0246609.			
PR	08-NOV-2000; 2000US-0246610.			
PR	08-NOV-2000; 2000US-0246611.			
PR	08-NOV-2000; 2000US-0246613.			
PR	17-NOV-2000; 2000US-0249207.			
PR	17-NOV-2000; 2000US-0249208.			
PR	17-NOV-2000; 2000US-0249209.			
PR	17-NOV-2000; 2000US-0249210.			
PR	17-NOV-2000; 2000US-0249211.			
PR	17-NOV-2000; 2000US-0249212.			
PR	17-NOV-2000; 2000US-0249213.			
PR	17-NOV-2000; 2000US-0249214.			
PR	17-NOV-2000; 2000US-0249215.			

OY 121 AWDYTDTRDGRVGEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADODGD 180
Db 136 AWDYTDTRDGRVGEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADODGD 195
OY 181 SMATRELTAFHPPEFPHMRDIVIAETLEDLRNKGQVQVEEYIADLYSAEPGEPEPA 240
Db 196 SMATRELTAFHPPEFPHMRDIVIAETLEDLRNKGQVQVEEYIADLYSAEPGEPEPA 255
OY 241 WYQTERQQFRDRLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Db 256 WYQTERQQFRDRLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 315
OY 301 EILGNWNVFVSQATNYGEDLTRHDEL 328
Db 316 EILGNWNVFVSQATNYGEDLTRHDEL 343

RESULT 13
AAW67852
ID AAW67852 standard; Protein; 328 AA.
XX
AC AAW67852;
XX
DT 25-MAR-1999 (first entry)
DE Human secreted protein encoded by gene 46 clone H5JBQ79.
XX Human;
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
XX
FH Key
FT Misc-difference 300
FT Misc-difference /label= unknown
FT Misc-difference 328
FT Misc-difference /label= unknown
XX
PN W09842738-A1.
XX
PD 01-OCT-1998.
XX
PF 19-MAR-1998; 98MO-US05311.
XX
PR 30-MAY-1997; 97US-0050937.
PR 21-MAR-1997; 97US-0041276.
PR 21-MAR-1997; 97US-0041277.
PR 21-MAR-1997; 97US-0041281.
PR 21-MAR-1997; 97US-0042344.
PR 30-MAY-1997; 97US-0048069.
PR 30-MAY-1997; 97US-0048094.
PR 30-MAY-1997; 97US-0048095.
PR 30-MAY-1997; 97US-0048096.
PR 30-MAY-1997; 97US-0048099.
PR 30-MAY-1997; 97US-0048131.
PR 30-MAY-1997; 97US-0048135.
PR 30-MAY-1997; 97US-0048154.
PR 30-MAY-1997; 97US-0048160.
PR 30-MAY-1997; 97US-0048186.
PR 30-MAY-1997; 97US-0048187.
PR 30-MAY-1997; 97US-0048188.
PR 30-MAY-1997; 97US-0048350.
PR 30-MAY-1997; 97US-0048351.
PR 30-MAY-1997; 97US-0048352.
PR 30-MAY-1997; 97US-0048355.
PR 05-AUG-1997; 97US-0054804.

(HUMA-) HUMAN GENOME SCI INC.
Brewer LA, Duan R, Ebner R, Ferrle AM, Florence KA,
Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;
Rosen CA, Ruben SM, Shi Y, Young P;
WPI; 1999-070066/06.
DR N-PSDB; AAX00656.
XX
New isolated human genes and the secreted polypeptides they encode -
useful for diagnosis and treatment of e.g. cancers, neurological
disorders, immune diseases, inflammation or blood disorders
Claim 11; Page 297-298; 385pp; English.
XX
This sequence represents a secreted human protein encoded by the gene
clone detailed in the descriptor line. The gene can be used to generate
fusion proteins by linking to the gene to a human immunoglobulin FC
portion (e.g. AAX00602) for increasing the stability of the fused
protein as compared to the human protein only.
XX
The invention relates to 87 novel genes and their fragments (nucleic
acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)
which are useful for preventing, treating or ameliorating medical
conditions e.g. by protein or gene therapy. Also, pathological
XX
polypeptides in a sample or by determining the amount of the new
polypeptides in a sample or by determining the presence of mutations in
XX
polynucleotides. Specific uses are described for each of the 87
XX
(see AAX00611 for described uses).
SQ Sequence 328 AA;
Query Match 99.4%; Score 1761; DB 20; Length 328;
Best Local Similarity 99.4%; Pred. No. 1.8e-154;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 MWPSVILLLLLRHGAQKPSDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAF 61
Db 1 MWPSVILLLLLRHGAQKPSDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAF 60
OY 62 REVAKFQDLTPESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHRSVSA 121
Db 61 REVAKFQDLTPESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHRSVSA 120
OY 122 WDTYTDTRDGRVGEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADODGD 181
Db 121 WDTYTDTRDGRVGEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADODGD 180
OY 182 MATRELTAFHPPEFPHMRDIVIAETLEDLRNKGQVQVEEYIADLYSAEPGEPEPA 241
Db 181 MATRELTAFHPPEFPHMRDIVIAETLEDLRNKGQVQVEEYIADLYSAEPGEPEPA 240
OY 242 VQTERQQFRDRLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 301
Db 241 VQTERQQFRDRLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
OY 302 ILGNWNVFVSQATNYGEDLTRHDEL 328
Db 301 ILGNWNVFVSQATNYGEDLTRHDEL 327

RESULT 14
AAG75587
ID AAG75587 standard; Protein; 240 AA.
XX
AC AAG75587;
XX
DT 03-SEP-2001 (first entry)
DE Human colon cancer antigen protein SEQ ID NO:6351.
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma.

XX Homo sapiens.
OS WO200122920-A2.
XX
XX
XX 05-APR-2001.
PD
XX 28-SEP-2000; 2000WO-US26524.
PF
XX 29-SEP-1999; 99US-0157137.
XX PR
XX 03-NOV-1999; 99US-0163280.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
PI
XX WPI; 2001-235357/24.
XX N-PSDB; AAH34992.
DR
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
PT
XX
XX Claim 11; Page 7803-7804; 9803pp; English.
PS
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing P.
CC Inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37195 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
XX Sequence 240 AA;
SQ
Query Match 55.2%; Score 978; DB 22; Length 240;
Best Local Similarity 92.9%; Pred. No. 3.3e-82;
Matches 184; Conservative 2; Mismatches 12; Indels 0; Gaps 0;
QY 131 GRVGWEELRNATYGHYAPGEEFHVDVDAETYYKMLARDERRFRVADQDGSMTREELTA 190
DB 43 GRASRVDRHAAHAAATGLGEEFHVDVDAETYYKMLARDERRFRVADQDGSMTREELTA 102
QY 191 FLHPEEPFMRDIVIAETLEDLRNKGYYQVVEEYIADLYSAPGEEPAWQTERQQFR 250
DB 103 FLHPEEPFMRDIVIAETLEDLRNKGYYQVVEEYIADLYSAPGEEPAWQTERQQFR 162
QY 251 DFRDLNKGHDLDGSEVGHWWLPPAQDQPLVEANHLHESDTDKDGRLSKAEILGNMFEV 310
DB 163 DFRDLNKGHDLDGSEVGHWWLPPAQDQPLVEANHLHESDTDKDGRLSKAEILGNMFEV 222
QY 311 GSQATNYGEDLTRHDEL 328
DB 223 GSQATNYGEDLTRHDEL 240
RESULT 15
AAW67906
ID AAW67906 standard; Protein: 184 AA.
XX

CC fusion proteins by linking to the gene to a human immunoglobulin Fc
CC portion (e.g. AAX00602) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 87 novel genes and their fragments (nucleic
CC acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC polypeptides in a sample or by determining the amount of the new
CC the new polynucleotides. Specific uses are described for each of the 87
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAX00611 for described uses).

xx SQ Sequence 184 AA;

Query Match 54.68; Score 967; DB 20; Length 184;
Best Local Similarity 97.3%; Pred. No. 2.3e-81;
Matches 179; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 MWRPSVLLLLLLLRHGAGKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFLG 61
Db 1 MWRPSVLLLLLLLRHGAGKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFLG 60
Qy 62 REVAKFEDQLTPESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 121
Db 61 REVAKFEDQLTPESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
Qy 122 WDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDEDAETKMKMLARDERRFRVADODGDS 181
Db 121 WDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDEDAETKMKMLARDERRFRVADODGDS 180
Qy 182 MATR 185
Db 181 MATR 184

Search completed: May 14, 2003, 10:42:56
Job time : 105.883 secs

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GenCore version 5.1.4.p5-4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:41:13 ; Search time 37,5132 Seconds
(without alignments)
257.262 Million cell updates/sec

Title: US-09-768-840-1

Perfect score: 1772

Sequence: 1 MMWRPSVLLLLLRHGAQG.....FVGSQATNYGDLTRHDEL 328

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1772	100.0	328	2	US-08-828-242-1
2	1772	100.0	328	2	US-08-910-927B-1
3	1772	100.0	328	4	US-09-206-499-1
4	1772	100.0	328	4	US-09-270-270-1
5	944	53.3	331	2	US-08-828-242-3
6	944	53.3	331	2	US-08-910-927B-5
7	944	53.3	331	4	US-09-206-499-3
8	944	53.3	331	4	US-09-270-270-5
9	938	52.9	325	2	US-08-828-242-4
10	938	52.9	325	4	US-09-206-499-4
11	842.5	47.5	315	2	US-08-910-927B-3
12	842.5	47.5	315	4	US-09-270-270-3
13	481	27.1	98	2	US-08-910-927B-6
14	481	27.1	98	4	US-09-270-270-6
15	456.5	25.8	317	2	US-08-555-722-8
16	456.5	25.8	317	4	US-09-384-301-8
17	362.5	20.5	220	2	US-08-840-683-8
18	134.5	7.6	276	3	US-09-048-889-4
19	128	7.2	456	1	US-08-464-164-2
20	128	7.2	456	1	US-08-338-057-2
21	128	7.2	456	2	US-08-668-416-2
22	124	7.0	146	3	US-08-963-409-1
23	122.5	6.9	619	3	US-08-813-150-6
24	118.5	6.7	145	4	US-08-720-625-5
25	117.5	6.6	642	2	US-08-818-253-2
26	117.5	6.6	642	4	US-08-818-252-2
27	117.5	6.6	652	2	US-08-818-253-4

28	117.5	6.6	652	4	US-08-818-252-4	Sequence 4, Appl1
29	114.5	6.5	642	2	US-08-818-253-6	Sequence 6, Appl1
30	114.5	6.5	642	4	US-08-818-252-6	Sequence 6, Appl1
31	114.5	6.5	656	2	US-08-818-253-8	Sequence 8, Appl1
32	114.5	6.5	656	4	US-08-818-252-8	Sequence 8, Appl1
33	112.5	6.3	179	3	US-08-764-563-4	Sequence 4, Appl1
34	111	6.3	257	4	US-09-399-913-16	Sequence 16, Appl1
35	111	6.3	257	4	US-09-399-913-16	Sequence 16, Appl1
36	108	6.1	270	4	US-09-399-913-18	Sequence 18, Appl1
37	108	6.1	270	4	US-09-398-731-18	Sequence 18, Appl1
38	107.5	6.1	150	4	US-09-329-909-2	Sequence 2, Appl1
39	107.5	6.1	160	2	US-08-602-941-1	Sequence 1, Appl1
40	107.5	6.1	160	3	US-08-961-264-1	Sequence 1, Appl1
41	107.5	6.1	160	4	US-09-442-099A-1	Sequence 1, Appl1
42	107.5	6.1	169	4	US-08-720-625-4	Sequence 4, Appl1
43	107.5	6.1	170	3	US-08-764-563-5	Sequence 5, Appl1
44	107	6.0	270	4	US-09-399-913-14	Sequence 14, Appl1
45	107	6.0	270	4	US-09-298-731-14	Sequence 14, Appl1

ALIGNMENTS

RESULT 1
US-08-828-242-1
; Sequence 1, Application US/08828242
; Patent No. 5871970 ✓
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L. **SAFE**
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CONUTUR01
; CLONE: 2509570
US-08-828-242-1

Query Match 100.0%; Score 1772; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-168;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CLONE: 922578
US-08-910-927B-1
Query Match 100.0%; Score 1772; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-168; Indels 0; Gaps 0;
Matches 328; Conservative 0; Mismatches 0;

QY 1 MMWRPSVLLLLLLLRRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDHDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLLLRRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDHDAHGNFYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 ANDTYDTRDGRGVGEELRNATYGHVAPGEEFHDVEDAETTKKMLARDERRFRVADQDGD 180
DB 121 ANDTYDTRDGRGVGEELRNATYGHVAPGEEFHDVEDAETTKKMLARDERRFRVADQDGD 180
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGDVYQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGDVYQVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQQFRDLNKGDLGSEVGHVWLPAPADQPLVEANHLHESDTRDKDGRLSKA 300
DB 241 WVQTERQQFRDLNKGDLGSEVGHVWLPAPADQPLVEANHLHESDTRDKDGRLSKA 300
QY 301 EILGNWMMFVGSQATNYGEDLTRHDEL 328
DB 301 EILGNWMMFVGSQATNYGEDLTRHDEL 328

RESULT 3
US-09-206-499-1
Sequence 1, Application US/09206499
Patent No. 6194385
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L. — SAME
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL CALCIUM-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,499
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,242
FILING DATE: 03/31/1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0261 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: single
LIBRARY: RATRNOT02

QY 1 MMWRPSVLLLLLLLRRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDHDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLLLRRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDHDAHGNFYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 ANDTYDTRDGRGVGEELRNATYGHVAPGEEFHDVEDAETTKKMLARDERRFRVADQDGD 180
DB 121 ANDTYDTRDGRGVGEELRNATYGHVAPGEEFHDVEDAETTKKMLARDERRFRVADQDGD 180
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGDVYQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGDVYQVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQQFRDLNKGDLGSEVGHVWLPAPADQPLVEANHLHESDTRDKDGRLSKA 300
DB 241 WVQTERQQFRDLNKGDLGSEVGHVWLPAPADQPLVEANHLHESDTRDKDGRLSKA 300
QY 301 EILGNWMMFVGSQATNYGEDLTRHDEL 328
DB 301 EILGNWMMFVGSQATNYGEDLTRHDEL 328

RESULT 2
US-08-910-927B-1
Sequence 1, Application US/08910927B
Patent No. 5976801
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,927B
FILING DATE: Hereewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0358 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: RATRNOT02

11/2/99
Different

3/16/99 8/8/97

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: CONUTUT01
CLONE: 2509570
US-09-206-499-1

Query Match 100.0%; Score 1772; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-168;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLRHGAQKSPDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
DB 1 MMWRPSVLLLLLRHGAQKSPDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
QY 61 GREVAKEDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
DB 61 GREVAKEDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRGVWEELRNATYGHYAPGEEFHDEDAETYYKMLARDERRFRVADQDGD 180
DB 121 AWDYTDTRDGRGVWEELRNATYGHYAPGEEFHDEDAETYYKMLARDERRFRVADQDGD 180
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKDGYVOVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKDGYVOVEEYIADLYSAEPGEEPA 240
QY 241 WVOTERQQRFRDLNKGHLGSEVGHVWLPAPADQPLVEANHLHESDTDKDGRLSKA 300
DB 241 WVOTERQQRFRDLNKGHLGSEVGHVWLPAPADQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNMNFVGSQATNYGDELTRHHDEL 328
DB 301 EILGNMNFVGSQATNYGDELTRHHDEL 328

RESULT 4

US-09-270-270-1
Sequence 1, Application US/09270270
Patent No. 6235477 5/22/01
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,270
FILING DATE: 3/16/99
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/910,927
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0358 US
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166

TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: RATRNOT02
CLONE: 922578
US-09-270-270-1

Query Match 100.0%; Score 1772; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-168;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLRHGAQKSPDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
DB 1 MMWRPSVLLLLLRHGAQKSPDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
QY 61 GREVAKEDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
DB 61 GREVAKEDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRGVWEELRNATYGHYAPGEEFHDEDAETYYKMLARDERRFRVADQDGD 180
DB 121 AWDYTDTRDGRGVWEELRNATYGHYAPGEEFHDEDAETYYKMLARDERRFRVADQDGD 180
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKDGYVOVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKDGYVOVEEYIADLYSAEPGEEPA 240
QY 241 WVOTERQQRFRDLNKGHLGSEVGHVWLPAPADQPLVEANHLHESDTDKDGRLSKA 300
DB 241 WVOTERQQRFRDLNKGHLGSEVGHVWLPAPADQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNMNFVGSQATNYGDELTRHHDEL 328
DB 301 EILGNMNFVGSQATNYGDELTRHHDEL 328

RESULT 5

US-08-828-242-3
Sequence 3, Application US/08828242
Patent No. 5871970
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL CALCIUM-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,242
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0261 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1262329
US-08-910-927B-5

Query Match 53.3%; Score 944; DB 2; Length 331;
Best Local Similarity 54.7%; Pred. No. 4.5e-86;
Matches 181; Conservative 51; Mismatches 75; Indels 24; Gaps 5;

Qy 7 VLLLLLLRHGAQKPS-----PDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEA 58
Db 16 LLLALLVAPRVLRKPTVRKERVVRPD-----SELGERPPED-NQSFQYDHEA 62
Qy 59 FLGREVAKFDPQLTPESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSV 118
Db 63 FLGRDSTFTDQLTPDESKEKLGKIVRID--NDGDFVTTTELKTWKRVQRYIFDNV 120
Qy 119 SAADWTYDTRDGRVGEELRNATYGHYAPG-EFFHDEVEDAETYYKKMLARDERRFRVADQ 177
Db 121 AKWKYDTRDGRVGEELRNATYGHYAPG-EFFHDEVEDAETYYKKMLARDERRFRVADQ 180
Qy 178 DGSMTAREELTAFLEHPEEFPHMRDVIATLELDNRKDGYYQVEEVIADLYSAEPGEE 237
Db 181 NGDLTATREETAFLEHPEEFPHMRDVIATLELDNRKDGYYQVEEVIADLYSAEPGEE 240
Qy 238 EPWVQTERQOFDRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSHESDTDKDGL 297
Db 241 EPDWVLSERQFNEFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSHESDTDKDGL 300
Qy 298 SKAELGNWNNFVGSQATNYGDLTRHDEL 328
Db 301 TKEILENNWNNFVGSQATNYGDLTKNHDEL 331

RESULT 7
US-09-206-499-3
Sequence 3, Application US/09206499
Patent No. 6194385
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL CALCIUM-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: Hereewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

REFERENCE/DOCKET NUMBER: PF-0261 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1262329
US-08-910-927B-5

Query Match 53.3%; Score 944; DB 2; Length 331;
Best Local Similarity 54.7%; Pred. No. 4.5e-86;
Matches 181; Conservative 51; Mismatches 75; Indels 24; Gaps 5;

Qy 7 VLLLLLLRHGAQKPS-----PDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEA 58
Db 16 LLLALLVAPRVLRKPTVRKERVVRPD-----SELGERPPED-NQSFQYDHEA 62
Qy 59 FLGREVAKFDPQLTPESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSV 118
Db 63 FLGRDSTFTDQLTPDESKEKLGKIVRID--NDGDFVTTTELKTWKRVQRYIFDNV 120
Qy 119 SAADWTYDTRDGRVGEELRNATYGHYAPG-EFFHDEVEDAETYYKKMLARDERRFRVADQ 177
Db 121 AKWKYDTRDGRVGEELRNATYGHYAPG-EFFHDEVEDAETYYKKMLARDERRFRVADQ 180
Qy 178 DGSMTAREELTAFLEHPEEFPHMRDVIATLELDNRKDGYYQVEEVIADLYSAEPGEE 237
Db 181 NGDLTATREETAFLEHPEEFPHMRDVIATLELDNRKDGYYQVEEVIADLYSAEPGEE 240
Qy 238 EPWVQTERQOFDRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSHESDTDKDGL 297
Db 241 EPDWVLSERQFNEFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSHESDTDKDGL 300
Qy 298 SKAELGNWNNFVGSQATNYGDLTRHDEL 328
Db 301 TKEILENNWNNFVGSQATNYGDLTKNHDEL 331

RESULT 6
US-08-910-927B-5
Sequence 5, Application US/08910927B
Patent No. 5976801
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: Hereewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:


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; APPLICATION NUMBER: US/09/206,499
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/828,242
; APPLICATION NUMBER: 03/31/1997
; FILING DATE: 03/31/1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1262329
; US-09-206-499-3

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Query Match          53.3%; Score 944; DB 4; Length 331;
Best Local Similarity 54.7%; Pred. No. 4.5e-86;
Matches 181; Conservative 51; Mismatches 75; Indels 24; Gaps 5;

QY 7 VLLLLLLRHGAQGRPS-----PDAGPHGQGRVHOAAPLSDAPHDHAGNFQYDHEA 58
Db 16 LLLALLVAPRVLRKPTVKRVVRPD-----SELGERPPED-NQSFQYDHEA 62
QY 59 FLGREVAKEFQQLTPESQARLGRIVDRMDRAGDGGWVSLAEIRAWIAHTQQRHIRDSV 118
Db 63 FLGKEDSKTFQQLTPDESKERLGIIVRID--NDGCGFVTEELKTWIKRVQRYIFDNV 120
QY 119 SAANDTDTDRGVRGVEELRNATYGHYAPG-EFFHDEDAEYTKMLARDERRFRVADQ 177
Db 121 AKVWKDYDRDKDDKISWEYKQATYGYLGNPAEFHDSDDHHTFKKMLPRDERRKAADL 180
QY 178 DGSNATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPGEE 237
Db 181 NGDLTATREETAFLHPEEPEHMKIIVLTLEDIDKNGDGFVDQDEYIADMFSEHNGP 240
QY 238 EPAWVQTERQOFRDLNKGDLGSEVGHVLPAPQOQPLVEANHLHESDTDKDGLR 297
Db 241 EPDWLSEREQFNEFRDLNKGDLKDKDEIRHWPILPDYDHAQAEARHLVYESDKNKDEKL 300
QY 298 SKAEILGNMNFVGSQATNYGDLTRHDEL 328
Db 301 TKEEILGNMNFVGSQATNYGDLTKNHDEL 331

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RESULT 8
US-09-270-270-5
; Sequence 5, Application US/09270270
; Patent No. 6235477
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,270
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,927
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1262329
; US-09-270-270-5

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Query Match          53.3%; Score 944; DB 4; Length 331;
Best Local Similarity 54.7%; Pred. No. 4.5e-86;
Matches 181; Conservative 51; Mismatches 75; Indels 24; Gaps 5;

QY 7 VLLLLLLRHGAQGRPS-----PDAGPHGQGRVHOAAPLSDAPHDHAGNFQYDHEA 58
Db 16 LLLALLVAPRVLRKPTVKRVVRPD-----SELGERPPED-NQSFQYDHEA 62
QY 59 FLGREVAKEFQQLTPESQARLGRIVDRMDRAGDGGWVSLAEIRAWIAHTQQRHIRDSV 118
Db 63 FLGKEDSKTFQQLTPDESKERLGIIVRID--NDGCGFVTEELKTWIKRVQRYIFDNV 120
QY 119 SAANDTDTDRGVRGVEELRNATYGHYAPG-EFFHDEDAEYTKMLARDERRFRVADQ 177
Db 121 AKVWKDYDRDKDDKISWEYKQATYGYLGNPAEFHDSDDHHTFKKMLPRDERRKAADL 180
QY 178 DGSNATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPGEE 237
Db 181 NGDLTATREETAFLHPEEPEHMKIIVLTLEDIDKNGDGFVDQDEYIADMFSEHNGP 240
QY 238 EPAWVQTERQOFRDLNKGDLGSEVGHVLPAPQOQPLVEANHLHESDTDKDGLR 297
Db 241 EPDWLSEREQFNEFRDLNKGDLKDKDEIRHWPILPDYDHAQAEARHLVYESDKNKDEKL 300
QY 298 SKAEILGNMNFVGSQATNYGDLTRHDEL 328
Db 301 TKEEILGNMNFVGSQATNYGDLTKNHDEL 331

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RESULT 9
US-08-828-242-4
; Sequence 4, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto

```


us-09-768-840-1-rai

Tue May 20 14:43:27 2003

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;
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
;
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/828,242
; APPLICATION NUMBER: 03/31/1997
; FILING DATE: 03/31/1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 220582
;
; US-08-828-242-4

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Query Match 52.9%; Score 938; DB 2; Length 325;
Best Local Similarity 55.2%; Pred. No. 1.7e-85;
Matches 181; Conservative 47; Mismatches 76; Indels 24; Gaps 5;

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QY 10 LLLLRHGAQKPS-----PDAGPHGQGRVHQAPLSDAPHDDAHGNFOYDHEAFLG 61
DB 13 LLLALVALRAKPTVRKRVPRD-----SELGERPPED-NQSFQYDHEAFLG 59
QY 62 REVAKFDPOLTPESQARLGRIVDRMDRAGDGVWSLAELRAWIAHTQOHRIRDSVSA 121
DB 60 KEDSKTFDQSPDSKSKERLGIIVDRID--SDGDLVTTTELKWKIKRVQKRYIYDNVAKV 117
QY 122 WDTYDTRDGRVGVWEELRNATYGHYAPG-EFHDVEDAEYKKMLARDERRFVADQGD 180
DB 118 WKDYDRDKDEKISWEYKQATYGYLGNPAEFHDSDDHHTFKMLPRDERRFKASDLGD 177
QY 181 SMATREELTAFHPPEEPHMRDIVIAETLEDLRNKGQYVQVEEYIADLYSAEPGEEPA 240
DB 178 LTATREETAFHPPEEFHMKIEVIVLETLEDIDKNGDFVDQDEYIADMFSHEDNGPEPD 237
QY 241 WYOTERQOQFRDLNKGDLGDSGVGHVWLPAPQOQPLVEANHLHESDTDKDGRLSKA 300
DB 238 WLSEREQNFDFRLNKGDKLDKDEIRHWILPQDYDHAQAEARHLVYESDKNKDEMLTKE 297
QY 301 EILGNWNVFVGSQATNYGEDLTRHDEL 328
DB 298 EILDNNMNVFVGSQATNYGEDLTRHDEL 325

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RESULT 10
US-09-206-499-4
; Sequence 4, Application US/09206499
; Patent No. 6194385
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

```

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RESULT 11
US-08-910-927B-3
; Sequence 3, Application US/08910927B
; Patent No. 5976801
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti

```

```

Query Match 52.9%; Score 938; DB 4; Length 325;
Best Local Similarity 55.2%; Pred. No. 1.7e-85;
Matches 181; Conservative 47; Mismatches 76; Indels 24; Gaps 5;

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QY 10 LLLLRHGAQKPS-----PDAGPHGQGRVHQAPLSDAPHDDAHGNFOYDHEAFLG 61
DB 13 LLLALVALRAKPTVRKRVPRD-----SELGERPPED-NQSFQYDHEAFLG 59
QY 62 REVAKFDPOLTPESQARLGRIVDRMDRAGDGVWSLAELRAWIAHTQOHRIRDSVSA 121
DB 60 KEDSKTFDQSPDSKSKERLGIIVDRID--SDGDLVTTTELKWKIKRVQKRYIYDNVAKV 117
QY 122 WDTYDTRDGRVGVWEELRNATYGHYAPG-EFHDVEDAEYKKMLARDERRFVADQGD 180
DB 118 WKDYDRDKDEKISWEYKQATYGYLGNPAEFHDSDDHHTFKMLPRDERRFKASDLGD 177
QY 181 SMATREELTAFHPPEEPHMRDIVIAETLEDLRNKGQYVQVEEYIADLYSAEPGEEPA 240
DB 178 LTATREETAFHPPEEFHMKIEVIVLETLEDIDKNGDFVDQDEYIADMFSHEDNGPEPD 237
QY 241 WYOTERQOQFRDLNKGDLGDSGVGHVWLPAPQOQPLVEANHLHESDTDKDGRLSKA 300
DB 238 WLSEREQNFDFRLNKGDKLDKDEIRHWILPQDYDHAQAEARHLVYESDKNKDEMLTKE 297
QY 301 EILGNWNVFVGSQATNYGEDLTRHDEL 328
DB 298 EILDNNMNVFVGSQATNYGEDLTRHDEL 325

```


APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,927B
FILING DATE: Hereewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0358 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADNOT03
CLONE: 1601793
US-08-910-927B-3

Query Match 47.5%; Score 842.5; DB 2; Length 315;
Best Local Similarity 50.5%; Pred. No. 5.6e-76;
Matches 161; Conservative 60; Mismatches 87; Indels 11; Gaps 4;
QY 8 LLLLLLHGAQGKPSDPAGPHGQGRVHQAPLSDAPHDDAHGNFYDHEAFLGREVAKE 67
Db 7 LMCLSLCTAFALSKPT-----EKKDRVHHEPQLSDKVHNDQAQ-SFDYDHDALGAEAKT 60
QY 68 FDLTPESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQORHIRDSVSAANDTYDT 127
Db 61 FDLTPESKERLGKIVSKID--GDKDGFVTVDELKDWIKFAKRWIYEDVERQWKHDL 118
QY 128 DRGRVGEELRNATYGHVAPGEEFHDVEDAETTKMLARDERRFRVADQDGSMTREE 187
Db 119 NEDGLVSWEEYKNATYGYVL---DDPPDDGFNYKQMVYDERFRKMDKDGDLIATKEE 175
QY 188 LTAFLPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPAWQTERQ 247
Db 176 FTAFLPEEYDKMDIVVQETMEDIDKNADGFDLDEEYIGDMYSHDGNTPDEPEWVKTERE 235
QY 248 QFRDRLNKGDLGSEYGHVLPAPQDQPLVEANHLHESDTDKDGRLSKAELGNWN 307
Db 236 QFVEFRDKNRDGMKDEETKDWILPSDYDHAEAEARHLVYESDQNKDGKLTKEEIVDKYD 295
QY 308 MFVGSQATNYGEDLTRHHD 326
Db 296 LFFVGSQATDFGEALVRHDE 314

RESULT 12
US-09-270-270-3

Sequence 3, Application US/09270270
Patent No. 6235477
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,270
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/910,927
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0358 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADNOT03
CLONE: 1601793
US-09-270-270-3

Query Match 47.5%; Score 842.5; DB 4; Length 315;
Best Local Similarity 50.5%; Pred. No. 5.6e-76;
Matches 161; Conservative 60; Mismatches 87; Indels 11; Gaps 4;
QY 8 LLLLLLHGAQGKPSDPAGPHGQGRVHQAPLSDAPHDDAHGNFYDHEAFLGREVAKE 67
Db 7 LMCLSLCTAFALSKPT-----EKKDRVHHEPQLSDKVHNDQAQ-SFDYDHDALGAEAKT 60
QY 68 FDLTPESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQORHIRDSVSAANDTYDT 127
Db 61 FDLTPESKERLGKIVSKID--GDKDGFVTVDELKDWIKFAKRWIYEDVERQWKHDL 118
QY 128 DRGRVGEELRNATYGHVAPGEEFHDVEDAETTKMLARDERRFRVADQDGSMTREE 187
Db 119 NEDGLVSWEEYKNATYGYVL---DDPPDDGFNYKQMVYDERFRKMDKDGDLIATKEE 175
QY 188 LTAFLPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPAWQTERQ 247
Db 176 FTAFLPEEYDKMDIVVQETMEDIDKNADGFDLDEEYIGDMYSHDGNTPDEPEWVKTERE 235
QY 248 QFRDRLNKGDLGSEYGHVLPAPQDQPLVEANHLHESDTDKDGRLSKAELGNWN 307
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QY 308 MFVGSQATNYGEDLTRHHD 326


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Db 296 LFVGSQATDEGEALVRHDE 314
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RESULT 13
US-08-910-927B-6
; Sequence 6, Application US/08910927B
; Patent No. 5976801
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,927B
; FILING DATE: Hereewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 780361
;
; US-08-910-927B-6
Query Match 27.1%; Score 481; DB 2; Length 98;
Best Local Similarity 93.7%; Pred. No. 1.le-40;
Matches 89; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Db 2 RDVAKEDQLTPESQARLGRIYDRMDLAGSDGWSLAALRAWIAHTQQRHIRDSVSA 61
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Qy 122 WDTYDTRDGRVGVWEELRNATYGHYAPGEFHDVE 156
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Db 62 WHTYDTRDGRVGVWEELRNATYGHYEPGEFHDVE 96
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RESULT 15
US-08-555-722-8
; Sequence 8, Application US/08555722
; Patent No. 5989804
; GENERAL INFORMATION:
; APPLICANT: Androphy, Elliot J.
; APPLICANT: Chen, Jason J.
; TITLE OF INVENTION: E6-BINDING PROTEINS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
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Job time : 39.5132 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2003, 10:43:07 ; Search time 31.7419 Seconds
(without alignments)
950.932 Million cell updates/sec

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Perfect score: 1772
Sequence: 1 MMWRPSVLLLLLRHGAQG.....FVGSQATNYCEDLRRHDEL 328

Scoring table: BLOSUM62

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Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA.*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1772	100.0	328	9	US-09-907-841-221
5	1772	100.0	328	9	US-09-904-011-221
6	1772	100.0	328	9	US-10-028-072-364
7	1772	100.0	328	9	US-09-906-742-221
8	1772	100.0	328	9	US-10-121-049-364
9	1772	100.0	328	9	US-10-123-904-364
10	1772	100.0	328	9	US-10-140-470-364
11	1772	100.0	328	9	US-09-906-838-221
12	1772	100.0	328	9	US-09-907-813-221
13	1772	100.0	328	9	US-10-175-746-364
14	1772	100.0	328	9	US-10-176-918-364
15	1772	100.0	328	9	US-10-176-921-364
16	1772	100.0	328	9	US-10-137-865-364
17	1772	100.0	328	9	US-10-140-474-364
18	1772	100.0	328	9	US-09-904-820-221
19	1772	100.0	328	9	US-09-904-820-221

20	1772	100.0	328	9	US-09-904-859-221	Sequence 221, App
21	1772	100.0	328	9	US-09-909-204-221	Sequence 221, App
22	1772	100.0	328	9	US-10-142-431-364	Sequence 364, App
23	1772	100.0	328	9	US-10-143-114-364	Sequence 364, App
24	1772	100.0	328	9	US-09-904-786-221	Sequence 221, App
25	1772	100.0	328	9	US-09-906-646-221	Sequence 221, App
26	1772	100.0	328	9	US-09-906-700-221	Sequence 221, App
27	1772	100.0	328	9	US-10-140-002-364	Sequence 364, App
28	1772	100.0	328	9	US-09-902-903-221	Sequence 221, App
29	1772	100.0	328	9	US-09-903-749A-221	Sequence 221, App
30	1772	100.0	328	9	US-09-903-786-221	Sequence 221, App
31	1772	100.0	328	9	US-10-142-419-364	Sequence 364, App
32	1772	100.0	328	9	US-09-902-736-221	Sequence 221, App
33	1772	100.0	328	9	US-09-904-119-221	Sequence 221, App
34	1772	100.0	328	9	US-09-904-956-221	Sequence 221, App
35	1772	100.0	328	9	US-09-907-794-221	Sequence 364, App
36	1772	100.0	328	9	US-10-123-262-364	Sequence 364, App
37	1772	100.0	328	9	US-09-902-692-221	Sequence 221, App
38	1772	100.0	328	9	US-09-903-520-221	Sequence 221, App
39	1772	100.0	328	9	US-09-903-943-221	Sequence 221, App
40	1772	100.0	328	9	US-09-904-462-221	Sequence 221, App
41	1772	100.0	328	9	US-09-907-925-221	Sequence 221, App
42	1772	100.0	328	9	US-10-121-050-364	Sequence 364, App
43	1772	100.0	328	9	US-10-141-755-364	Sequence 364, App
44	1772	100.0	328	9		
45	1772	100.0	328	9		

ALIGNMENTS

RESULT 1

Sequence 221, Application US/09905291A
Patent No. US20020160374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222

APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-09-902-853-221

Query Match 100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLRHGAGKSPDAGPHGQGRVHOAAAPLSDAPHDHDAHGFQYDHEAFL 60
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Db 61 GREVAEFQLPESQARLGRVDMRDAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120

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Db 121 AWDYTDTRDGRVGEELNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFVADQGD 180

QY 181 SMATREELTAFLPEEPFPHRDIVIAETLEDLRNKGDVVQVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLPEEPFPHRDIVIAETLEDLRNKGDVVQVEEYIADLYSAEPGEEPA 240

QY 241 WQOTERQOFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHSDTDKDLRLSKA 300
Db 241 WQOTERQOFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHSDTDKDLRLSKA 300

QY 301 EILGNWNNFVGSQATNGEDLTRHDEL 328
Db 301 EILGNWNNFVGSQATNGEDLTRHDEL 328

RESULT 2
US-09-902-853-221
; Sequence 221, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.

QY 61 GREVAKEFDQLTPEESQARGLRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARGLRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
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Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADAETYYKKMLARDERRFRVADODGD 180
QY 181 SMATREELTAFLHPPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPGEEPA 240
Db 181 SMATREELTAFLHPPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPGEEPA 240
QY 241 WQTEROQFRDRLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WQTEROQFRDRLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNMNFVGSQATNYGDLTRHDEL 328
Db 301 EILGNMNFVGSQATNYGDLTRHDEL 328

RESULT 3

US-09-907-824-221
; Sequence 221, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Grittsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-221

Query Match

Best Local Similarity 100.0%; Score 1772; DB 9; Length 328;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MMWRPSVLLLLLLRHGAGKPSDPAGPHGQGRVHQRAAPLSDAPHDHAGNFQYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARGLRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARGLRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADAETYYKKMLARDERRFRVADODGD 180
Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADAETYYKKMLARDERRFRVADODGD 180
QY 181 SMATREELTAFLHPPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPGEEPA 240
Db 181 SMATREELTAFLHPPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPGEEPA 240
QY 241 WQTEROQFRDRLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WQTEROQFRDRLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNMNFVGSQATNYGDLTRHDEL 328
Db 301 EILGNMNFVGSQATNYGDLTRHDEL 328

RESULT 4

US-09-907-841-221
; Sequence 221, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Grittsen, Mary E.
; APPLICANT: Goddard, A.

us-09-768-840-1.rapb

Tue May 20 14:43:28 2003

```

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-841-221

Query Match          100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2,1e-143;
Matches: 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Db 1 MMWRPSVLLLLLLRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFL 60
   |||||

QY 61 GREVAKFEQLTTPESQARLGRIVDRMDRAGDGDGWSVLAELRAWTAHTQQRHIRDSVSA 120
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Db 61 GREVAKFEQLTTPESQARLGRIVDRMDRAGDGDGWSVLAELRAWTAHTQQRHIRDSVSA 120
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QY 121 AWDTYTDRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
   |||||
Db 121 AWDTYTDRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
   |||||

QY 181 SMATREELTAFLHPHEFFPMRDIVIAETLEDLRNKGYYVQVEEYIADLYSAPGEEPPA 240
   |||||
Db 181 SMATREELTAFLHPHEFFPMRDIVIAETLEDLRNKGYYVQVEEYIADLYSAPGEEPPA 240
   |||||

QY 241 WVQTERQQFRDFRLNKGHLDDGSEVGHWWLPPAQDQPLVEANHLHESDTDKDGRLSKA 300
   |||||
Db 241 WVQTERQQFRDFRLNKGHLDDGSEVGHWWLPPAQDQPLVEANHLHESDTDKDGRLSKA 300
   |||||

QY 301 EILGNMNFVGSQATNYGDELTRHDEL 328
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; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-221

Query Match
Best Local Similarity 100.0%; Score 1772; DB 9; Length 328;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLLHGAAGKSPDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
Db 1 MMWRPSVLLLLLLLHGAAGKSPDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
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Db 181 SMATREELTAFLHPPEEFHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
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Db 241 WYQTERQOFRDRLNKGCHLDGSEVGHVLPAPQDQPLVEANLLHESDPTDKDGRLSKA 300
QY 301 ETLGNMNFVGSQATNYGCDLTRHDEL 328
Db 301 ETLGNMNFVGSQATNYGCDLTRHDEL 328

RESULT 6
US-10-028-072-364
; Sequence 364, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
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; PRIOR FILING DATE: 1997-09-17
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;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07

Query Match 100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLHGAQKPSDPAGPHCGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLHGAQKPSDPAGPHCGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60

QY 61 GREVAKFEDLTPEESQARLGRIVDRMDRAGDGDGVWSLAELRAWTIAHTQQRHRSVSA 120
DB 61 GREVAKFEDLTPEESQARLGRIVDRMDRAGDGDGVWSLAELRAWTIAHTQQRHRSVSA 120

QY 121 AWDYTDTRDRGVRGWEELRNATYGHYAPGEFHDVEADTYKKMLARDERRFVADQGD 180
DB 121 AWDYTDTRDRGVRGWEELRNATYGHYAPGEFHDVEADTYKKMLARDERRFVADQGD 180

QY 181 SMATREELTAFHPPEEPHMRDIVIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFHPPEEPHMRDIVIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEPA 240

QY 241 WVQTERQOFRDLNKDGLDSEVGHVWLPQAQDQPLVEANHLHSHSDTKDGRLSKA 300
DB 241 WVQTERQOFRDLNKDGLDSEVGHVWLPQAQDQPLVEANHLHSHSDTKDGRLSKA 300

QY 301 EILGNMFMVGSQATNYGEDLTRHDEL 328
DB 301 EILGNMFMVGSQATNYGEDLTRHDEL 328

RESULT 7
US-09-906-742-221
; Sequence 221, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-742-221

Query Match 100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2,1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60

QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQORHIRDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQORHIRDSVSA 120

QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEAETTKMLARDERRFRVADQGD 180
DB 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEAETTKMLARDERRFRVADQGD 180

QY 181 SMATREELTAFLLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPGEEPA 240
DB 181 SMATREELTAFLLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPGEEPA 240

QY 241 WYOTERQOQFRDRLDKNGHLDGSEVGHVWLPAPQOQPLVEANHLHESDTDKDGRLSKA 300
DB 241 WYOTERQOQFRDRLDKNGHLDGSEVGHVWLPAPQOQPLVEANHLHESDTDKDGRLSKA 300

QY 301 EILGNMNFVGSQATNYGEDLTRHDEL 328
DB 301 EILGNMNFVGSQATNYGEDLTRHDEL 328

RESULT 8

US-10-121-049-364
Sequence 364, Application US/10121049
Publication No. US2003002239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 364
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-10-121-049-364

Query Match 100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2,1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60

QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQORHIRDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQORHIRDSVSA 120

QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEAETTKMLARDERRFRVADQGD 180
DB 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEAETTKMLARDERRFRVADQGD 180

QY 181 SMATREELTAFLLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPGEEPA 240
DB 181 SMATREELTAFLLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPGEEPA 240

QY 241 WYOTERQOQFRDRLDKNGHLDGSEVGHVWLPAPQOQPLVEANHLHESDTDKDGRLSKA 300
DB 241 WYOTERQOQFRDRLDKNGHLDGSEVGHVWLPAPQOQPLVEANHLHESDTDKDGRLSKA 300

QY 301 EILGNMNFVGSQATNYGEDLTRHDEL 328
DB 301 EILGNMNFVGSQATNYGEDLTRHDEL 328

APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 364
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-470-364

Query Match 100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLLRHGAQKSPDAGHGQGRVHQAAPLSDAPHDHDAHGNFYDHEAFL 60
Db 1 MMWRPSVLLLLLLLRHGAQKSPDAGHGQGRVHQAAPLSDAPHDHDAHGNFYDHEAFL 60
QY 61 GREVAKEFDOLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDOLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAEYKKMLARDERRFRVADQGD 180
Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAEYKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQOFRDRLNKDGLDSEVGHVWLPVPAQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WVQTERQOFRDRLNKDGLDSEVGHVWLPVPAQDQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328
Db 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328

RESULT 11
US-09-906-838-221
Sequence 221, Application US/09906838
Publication No. US20030027143A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 364
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-10-123-904-364

Query Match 100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLLRHGAQKSPDAGHGQGRVHQAAPLSDAPHDHDAHGNFYDHEAFL 60
Db 1 MMWRPSVLLLLLLLRHGAQKSPDAGHGQGRVHQAAPLSDAPHDHDAHGNFYDHEAFL 60
QY 61 GREVAKEFDOLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDOLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAEYKKMLARDERRFRVADQGD 180
Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAEYKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQOFRDRLNKDGLDSEVGHVWLPVPAQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WVQTERQOFRDRLNKDGLDSEVGHVWLPVPAQDQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328
Db 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328

RESULT 10
US-10-140-470-364
Sequence 364, Application US/10140470
Publication No. US20030022331A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,838
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-838-221

Query Match 100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMWRPVLVLLLLLRHGAQKPSDPAGPHGGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
DB 1 MMWRPVLVLLLLLRHGAQKPSDPAGPHGGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
QY 61 GREVAKFDQLTPESQARLGRIYDRMDRAGDGDGWYSLAELRAWIAHTQORHROSVA 120
DB 61 GREVAKFDQLTPESQARLGRIYDRMDRAGDGDGWYSLAELRAWIAHTQORHROSVA 120

QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
DB 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEERPA 240
DB 181 SMATREELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEERPA 240
QY 241 WVQTERQQFRDRLNKNKDLGSGEYGHVLPAPQDPLVEANHLHESDTRKDLRLSKA 300
DB 241 WVQTERQQFRDRLNKNKDLGSGEYGHVLPAPQDPLVEANHLHESDTRKDLRLSKA 300
QY 301 EILGNMFMVGSQATNYGEDLRRHDEL 328
DB 301 EILGNMFMVGSQATNYGEDLRRHDEL 328
RESULT 12
US-09-907-613-221
Sequence 221, Application US/09907613
Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,613
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313

Tue May 20 14:43:28 2003

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; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-613-221

Query Match      100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLRHGAQGPSDPAGPHGQGRVHQAPLSDAPHDHDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLLRHGAQGPSDPAGPHGQGRVHQAPLSDAPHDHDAHGNFYDHEAFL 60
QY 61 GREVAKEFDQLTPTESQARLGRIVDMDRAGDGDGWSLAELRAWIAHTQORHTRDSVSA 120
DB 61 GREVAKEFDQLTPTESQARLGRIVDMDRAGDGDGWSLAELRAWIAHTQORHTRDSVSA 120
QY 121 AMDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERFRVADQGD 180
DB 121 AMDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERFRVADQGD 180
QY 181 SMATREELTAFLLHPEEFPHMRDIVIAETLEDLDRNKDGYGVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLLHPEEFPHMRDIVIAETLEDLDRNKDGYGVQVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQQRFRDLNKGHLSDGSEVGHVWLPDPAQDQPLVEANHLLHESDTRDKGRLSKA 300
DB 241 WVQTERQQRFRDLNKGHLSDGSEVGHVWLPDPAQDQPLVEANHLLHESDTRDKGRLSKA 300
QY 301 EILGNMFMVGSQATNYGDLTRHDEL 328
DB 301 EILGNMFMVGSQATNYGDLTRHDEL 328

RESULT 13
US-09-907-942-221
; Sequence 221, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavina, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
```

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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-942-221

Query Match      100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLRHGAQGPSDPAGPHGQGRVHQAPLSDAPHDHDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLLRHGAQGPSDPAGPHGQGRVHQAPLSDAPHDHDAHGNFYDHEAFL 60
QY 61 GREVAKEFDQLTPTESQARLGRIVDMDRAGDGDGWSLAELRAWIAHTQORHTRDSVSA 120
DB 61 GREVAKEFDQLTPTESQARLGRIVDMDRAGDGDGWSLAELRAWIAHTQORHTRDSVSA 120
QY 121 AMDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERFRVADQGD 180
DB 121 AMDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERFRVADQGD 180
QY 181 SMATREELTAFLLHPEEFPHMRDIVIAETLEDLDRNKDGYGVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLLHPEEFPHMRDIVIAETLEDLDRNKDGYGVQVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQQRFRDLNKGHLSDGSEVGHVWLPDPAQDQPLVEANHLLHESDTRDKGRLSKA 300
```


Db 241 WYOTERQQRFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTRHDEL 328
QY 301 EILGNMNFVGSQATNYGDLTRHDEL 328
Db 301 EILGNMNFVGSQATNYGDLTRHDEL 328

RESULT 14

US-10-175-746-364
; Sequence 364, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C353

; CURRENT APPLICATION NUMBER: US/10/175,746

; CURRENT FILING DATE: 2002-06-19

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 364

; LENGTH: 328

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-175-746-364

Query Match 100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2,1e-143;

Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLLRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNYDHEAFL 60
Db 1 MMWRPSVLLLLLLLRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNYDHEAFL 60

QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWTIAHTQQRHSDVSVA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWTIAHTQQRHSDVSVA 120

QY 121 AWDTYDTRDRGRVGEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
Db 121 AWDTYDTRDRGRVGEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180

QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKGQYVQVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKGQYVQVEEYIADLYSAEPGEEPA 240

QY 241 WYOTERQQRFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTRHDEL 328
Db 241 WYOTERQQRFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTRHDEL 328

QY 301 EILGNMNFVGSQATNYGDLTRHDEL 328
Db 301 EILGNMNFVGSQATNYGDLTRHDEL 328

RESULT 15

US-10-176-918-364

; Sequence 364, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C382

; CURRENT APPLICATION NUMBER: US/10/176,918

; CURRENT FILING DATE: 2002-06-20

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 364

; LENGTH: 328

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-918-364

Query Match 100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2,1e-143;

Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLLRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNYDHEAFL 60
Db 1 MMWRPSVLLLLLLLRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNYDHEAFL 60

QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWTIAHTQQRHSDVSVA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWTIAHTQQRHSDVSVA 120

QY 121 AWDTYDTRDRGRVGEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
Db 121 AWDTYDTRDRGRVGEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180

QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKGQYVQVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKGQYVQVEEYIADLYSAEPGEEPA 240

QY 241 WYOTERQQRFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTRHDEL 328
Db 241 WYOTERQQRFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTRHDEL 328

QY 301 EILGNMNFVGSQATNYGDLTRHDEL 328
Db 301 EILGNMNFVGSQATNYGDLTRHDEL 328

Search completed: May 14, 2003, 10:47:54
Job time : 34.7419 secs

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XX PS Claim 1; Page 42-43; 60pp; English.

XX XX The present sequence is a new human calcium binding protein (HCBP).

CC CC A pharmaceutical composition which includes the HCBP protein is claimed

CC CC and can be added directly to cells in vivo to promote regeneration or

CC CC differentiation of cells. HCBP can also be added to cells, cell lines,

CC CC tissue or organ culture to stimulate cell proliferation for heterologous

CC CC and autologous transplantation. The cells can be selected for their

CC CC ability to inhibit development of an infection or to correct a genetic

CC CC HCBP can be administered to a subject to treat or prevent a disorder

CC CC associated with cell proliferation e.g. many cancers including

CC CC adenocarcinoma, leukemia, lymphoma, melanoma, sarcoma and particularly

CC CC cancers of bladder, bone, brain, heart, kidney, liver. Antibodies

CC CC specific for HCBP may be used directly as an antagonist or indirectly as

CC CC a targeting or delivery mechanism for delivering pharmaceutical agents

CC CC to cell or tissue which express protein HCBP. A method is claimed for

CC CC treating or preventing a disorder associated with cell proliferation

CC CC which involves adding pharmaceutical composition of antagonist of HCBP.

XX XX

XX SQ Sequence 328 AA;

Query Match 100.0%; Score 328; DB 19; Length 328;

Best Local Similarity 100.0%; Pred. No. 4.9e-295; Indels 0; Gaps 0;

Matches 328; Conservative 0; Mismatches 0;

QY 1 MMWRPSVLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSADPHDDAHGNGFYDHEAFL 60

DB 1 MMWRPSVLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSADPHDDAHGNGFYDHEAFL 60

QY 61 GREVAKEFDLTPEESQARLGRIIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120

DB 61 GREVAKEFDLTPEESQARLGRIIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120

QY 121 AWDTYDTRDGRVGYWEELRNATYGHVAPGEEDHVEDAETFKKMLARDERRFRVADQDGD 180

DB 121 AWDTYDTRDGRVGYWEELRNATYGHVAPGEEDHVEDAETFKKMLARDERRFRVADQDGD 180

QY 181 SMATREELTAFLHPEEPHMRDVIATLEDDLRNKGDVQVEEYIADLYSAEPGEEPPA 240

DB 181 SMATREELTAFLHPEEPHMRDVIATLEDDLRNKGDVQVEEYIADLYSAEPGEEPPA 240

QY 241 WQTERQQFRDLNKGDLGSEVGHVWVLPAPQDQPLVEANHLHESDTDKDGLSKA 300

DB 241 WQTERQQFRDLNKGDLGSEVGHVWVLPAPQDQPLVEANHLHESDTDKDGLSKA 300

QY 301 EILGNWNMFVGSQATNYGDELTRHDEL 328

DB 301 EILGNWNMFVGSQATNYGDELTRHDEL 328

RESULT 2

AA13382

ID AA13382 standard; Protein; 328 AA.

XX XX

AC AA13382;

XX XX

DT 25-JUN-1999 (first entry)

XX XX

DE Amino acid sequence of protein PRO272.

XX XX

KW Secreted protein; transmembrane protein; human; enterocolitis;

KW Zollinger-Ellison syndrome; gastrointestinal ulceration;

KW congenital microvillus atrophy; skin disease; cell growth;

KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;

KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;

KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;

KW anti-thrombotic; wound healing; tissue repair.

OS Homo sapiens.

XX XX

PN WO914328-A2.

XX PD 25-MAR-1999.

XX PF 16-SEP-1998; 98WO-US19330.

XX XX

XX 25-NOV-1997; 97US-0066840.

PR 17-SEP-1997; 97US-0059113.

PR 17-SEP-1997; 97US-0059115.

PR 17-SEP-1997; 97US-0059117.

PR 17-SEP-1997; 97US-0059119.

PR 17-SEP-1997; 97US-0059121.

PR 17-SEP-1997; 97US-0059122.

PR 17-SEP-1997; 97US-0059184.

PR 18-SEP-1997; 97US-0059263.

PR 18-SEP-1997; 97US-0059266.

PR 15-OCT-1997; 97US-006125.

PR 17-OCT-1997; 97US-0062285.

PR 17-OCT-1997; 97US-0062287.

PR 21-OCT-1997; 97US-0063486.

PR 24-OCT-1997; 97US-0062814.

PR 24-OCT-1997; 97US-0062816.

PR 24-OCT-1997; 97US-0063045.

PR 24-OCT-1997; 97US-0063120.

PR 24-OCT-1997; 97US-0063121.

PR 24-OCT-1997; 97US-0063127.

PR 27-OCT-1997; 97US-0063128.

PR 27-OCT-1997; 97US-0063329.

PR 27-OCT-1997; 97US-0063327.

PR 28-OCT-1997; 97US-0063541.

PR 28-OCT-1997; 97US-0063542.

PR 28-OCT-1997; 97US-0063544.

PR 28-OCT-1997; 97US-0063549.

PR 28-OCT-1997; 97US-0063550.

PR 28-OCT-1997; 97US-0063564.

PR 29-OCT-1997; 97US-0063435.

PR 29-OCT-1997; 97US-0063704.

PR 29-OCT-1997; 97US-0063732.

PR 29-OCT-1997; 97US-0063738.

PR 29-OCT-1997; 97US-0063734.

PR 29-OCT-1997; 97US-0064215.

PR 29-OCT-1997; 97US-0063735.

PR 31-OCT-1997; 97US-0063870.

PR 31-OCT-1997; 97US-0064103.

PR 03-NOV-1997; 97US-0064248.

PR 07-NOV-1997; 97US-0064809.

PR 12-NOV-1997; 97US-0065186.

PR 17-NOV-1997; 97US-0065846.

PR 18-NOV-1997; 97US-0065693.

PR 21-NOV-1997; 97US-0066120.

PR 21-NOV-1997; 97US-0066364.

PR 24-NOV-1997; 97US-0066772.

PR 24-NOV-1997; 97US-0066466.

PR 24-NOV-1997; 97US-0066770.

PR 24-NOV-1997; 97US-0066511.

PR 24-NOV-1997; 97US-0066453.

XX XX

PA (GETH) GENENTECH INC.

XX XX

PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;

XX XX

DR WPI; 1999-229533/19.

DR N-PSDB; AAX52253.

XX XX

XX New isolated human genes and polypeptides used in, e.g. treatment of

PT gastrointestinal ulceration

XX XX

PS Claim 12; Fig 80; 320pp; English.

XX XX

CC AAY13344-403 represent secreted and transmembrane human proteins.

CC The cDNA sequences are obtained from cDNA libraries, prepared from

CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.

CC The encoded polypeptides have specific uses based on their homology to

CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders

CC associated with the preservation and maintenance of gastrointestinal
 CC mucosa and the repair of acute and chronic mucosal lesions
 CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
 CC ulceration and congenital microvillus atrophy), skin diseases associated
 CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
 CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),
 CC potent effects on cell growth and development, diseases related to
 CC growth or survival of nerve cells including Parkinson's disease,
 CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as
 CC a target for anti-tumor drugs. PRO533 may be used in the treatment
 CC of Usher Syndrome or Atrophia areata; PRO269 can be used as an
 CC anti-thrombotic agent; PRO287 polypeptides and portions may have
 CC therapeutic applications in wound healing and tissue repair; PRO317 can
 CC be used for treating problems of the kidney, uterus, endometrium, blood
 CC vessels, or related tissue, e.g. in the heart of genital tract.

XX Sequence 328 AA;

Query Match 100.0%; Score 328; DB 20; Length 328;
 Best Local Similarity 100.0%; Pred. No. 4.9e-295;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
 DB 1 MMWRPSVLLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60

QY 61 GREVAKEFDOLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWTQQRHIRDSVSA 120
 DB 61 GREVAKEFDOLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWTQQRHIRDSVSA 120

QY 121 AWDTYDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETTKMLARDERRFRVADQGD 180
 DB 121 AWDTYDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETTKMLARDERRFRVADQGD 180

QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGYVQVEEYIADLYSAEPGEEPA 240
 DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGYVQVEEYIADLYSAEPGEEPA 240

QY 241 WYQTERQQRFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTRDKGRLSKA 300
 DB 241 WYQTERQQRFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTRDKGRLSKA 300

QY 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328
 DB 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328

RESULT 3
 AAY00916

XX ID AAY00916 standard; Protein; 328 AA.

XX AC AAY00916;

XX XX 28-MAY-1999 (first entry)

XX Human reticulocalbin gamma protein sequence.

XX Human; reticulocalbin gamma; RCNgamma; reticulocalbin delta; RCndelta;
 KW developmental disorder; neoplastic disorder; immunological disorder;
 KW infection.

XX OS Homo sapiens.

XX PN WO9907849-A2.

XX PD 18-FEB-1999.

XX XX 05-AUG-1998; 98WO-US16259.

XX PF 08-AUG-1997; 97US-0910927.

XX PR (INCY-) INCYTE PHARM INC.

XX PA

XX

PI Bandman O, Corley NC, Hillman JL, Lal P, Shah P;

XX WPI; 1999-180492/15.

DR N-PSDB; AAX27229.

XX New human reticulocalbin isoforms - useful to diagnose, prevent,
 PT and treat infectious, developmental, neoplastic, and immunological
 PT disorders

XX Claim 1; Fig 1; 82pp; English.

XX This sequence is the human reticulocalbin gamma (RCNgamma) of the
 CC invention. RCNgamma and RCndelta are used to treat an infectious or
 CC developmental disorder, and antagonists of them are used to treat a
 CC neoplastic or immunological disorder. Infectious disorders include e.g.
 CC pneumonia, lymphocytic choriomeningitis, Hantavirus, chronic bronchitis,
 CC mumps, rhinovirus, poliovirus, coxsackie-virus, influenza, cancer, measles,
 CC fever, HIV, rabies, gastroenteritis, and rubella, encephalitis, and
 CC bacterial, fungal, parasitic, protozoal, or helminthic infections.
 CC Development disorders include e.g. renal tubular acidosis, anaemia,
 CC Cushing's syndrome, achondroplastic dwarfism, epilepsy, gonadal
 CC dysgenesis, hereditary neuropathies such as Charcot-Marie-Tooth disease,
 CC and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders
 CC such as Sydenham's chorea and cerebral palsy, spinal bifida, and
 CC congenital glaucoma, cataract, or sensorineural hearing loss. Neoplastic
 CC disorders include e.g. adenocarcinoma, leukaemia, lymphoma, melanoma,
 CC myeloma, sarcoma and teratocarcinoma. Overexpression of reticulocalbin
 CC mRNA has been associated with increased metastatic properties of
 CC three human breast cancer lines.

XX Sequence 328 AA;

Query Match 100.0%; Score 328; DB 20; Length 328;
 Best Local Similarity 100.0%; Pred. No. 4.9e-295;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
 DB 1 MMWRPSVLLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60

QY 61 GREVAKEFDOLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWTQQRHIRDSVSA 120
 DB 61 GREVAKEFDOLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWTQQRHIRDSVSA 120

QY 121 AWDTYDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETTKMLARDERRFRVADQGD 180
 DB 121 AWDTYDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETTKMLARDERRFRVADQGD 180

QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGYVQVEEYIADLYSAEPGEEPA 240
 DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGYVQVEEYIADLYSAEPGEEPA 240

QY 241 WYQTERQQRFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTRDKGRLSKA 300
 DB 241 WYQTERQQRFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTRDKGRLSKA 300

QY 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328
 DB 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328

RESULT 4

AAB33424

XX ID AAB33424 standard; Protein; 328 AA.

XX AC AAB33424;

XX XX 29-JAN-2001 (first entry)

XX Human PRO272 protein UNQ239 SEQ ID NO:51.

XX DE

XX XX

Tue May 20 14:43:20 2003

Human; immune related disease; diagnosis; antiinflammatory; cardiant;
dermatologic; antiarthritic; antirheumatic; immunosuppressive;
haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
osteoarthritic; spondyloarthropathy; systemic sclerosis; sarcoidosis;
idiopathic inflammatory myopathy; Sjogren's syndrome; rheumatoid arthritis;
systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
autoimmune thrombocytopenia; immune-mediated renal disease;
demyelinating disease; hepatobiliary disease; Whipple's disease;
inflammatory bowel disease; gluten-sensitive enteropathy;
autoimmune disease; immune-mediated skin disease; allergic disease;
immunological disease; transplantation associated disease;
graft rejection; graft-versus-host-disease.

Homo sapiens.

WO200053758-A2.

14-SEP-2000.

02-MAR-2000; 2000WO-US05841.

08-MAR-1999; 99WO-US05028.

10-MAR-1999; 99US-0123618.

12-MAR-1999; 99US-0123957.

23-MAR-1999; 99US-0125775.

12-APR-1999; 99US-0128849.

20-APR-1999; 99WO-US08615.

28-APR-1999; 99US-0131445.

04-MAY-1999; 99US-0132371.

14-MAY-1999; 99US-0134287.

02-JUN-1999; 99WO-US12252.

23-JUN-1999; 99US-0141037.

20-JUL-1999; 99US-0144758.

26-JUL-1999; 99US-0145698.

28-JUL-1999; 99US-0146222.

01-SEP-1999; 99WO-US20111.

08-SEP-1999; 99WO-US20594.

13-SEP-1999; 99WO-US20944.

15-SEP-1999; 99WO-US21090.

15-SEP-1999; 99WO-US21547.

05-OCT-1999; 99WO-US23089.

29-OCT-1999; 99US-0162506.

29-NOV-1999; 99WO-US28214.

30-NOV-1999; 99WO-US28313.

30-NOV-1999; 99WO-US28409.

01-DEC-1999; 99WO-US28301.

01-DEC-1999; 99WO-US28634.

02-DEC-1999; 99WO-US28551.

02-DEC-1999; 99WO-US28564.

02-DEC-1999; 99WO-US28565.

16-DEC-1999; 99WO-US30095.

PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

PS Claim 33; Fig 22; 309pp; English..

XX The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary and Whipple's disease, bowel disease, gluten-sensitive enteropathy and allergic diseases, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. RAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAC33414 to AAC33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

XX Sequence 328 AA;

SQ Query Match 100.0%; Score 328; DB 21; Length 328;

Best Local Similarity 100.0%; Pred. No. 4.9e-295; Indels 0; Gaps 0;

Matches 328; Conservative 0; Mismatches 0;

QY ° 1 MMWRPSVLLLLLHGAQKQSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60

Db 1 MMWRPSVLLLLLHGAQKQSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60

QY 61 GREVAKFQDLTPESQARLGRIVDRMDRAGDGGWVSLAEFLAWTAHTQORHRSVSA 120

Db 61 GREVAKFQDLTPESQARLGRIVDRMDRAGDGGWVSLAEFLAWTAHTQORHRSVSA 120

QY 121 AWDTYDTRDGRVGEELRNATYGHYAPGEFHDVEADATYKKMLARDERRFRVADODGD 180

Db 121 AWDTYDTRDGRVGEELRNATYGHYAPGEFHDVEADATYKKMLARDERRFRVADODGD 180

QY 181 SMATREELTAFLHPEEFPHMRDIVIAETLEDLRNKGIVQVVEYIADLYSAEPEEPA 240

Db 181 SMATREELTAFLHPEEFPHMRDIVIAETLEDLRNKGIVQVVEYIADLYSAEPEEPA 240

QY 241 WYQTERQDFRDLNKGHLGDSVGHVLPAPQDQPLVEANHLHESDTPDKGRLSKA 300

Db 241 WYQTERQDFRDLNKGHLGDSVGHVLPAPQDQPLVEANHLHESDTPDKGRLSKA 300

QY 301 EILGNMNFVGSQATNYGEDLTRHDEL 328

Db 301 EILGNMNFVGSQATNYGEDLTRHDEL 328

RESULT 5

AA53640

ID AA53640 standard; Protein; 328 AA.

XX AA53640;

XX 22-FEB-2000 (first entry)

XX A bone marrow secreted protein designated BMS37.

XX Bone marrow secreted protein; bone marrow stromal cell; cytokine;
KW cell proliferation; cell differentiation; hematopoiesis; anaemia;
KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
KW erythroid progenitor cell; colony stimulating factor; granulocyte;
KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
KW platelet disorder; thrombocytopenia; hematopoietic stem cell;
KW stem cell disorder; aplastic anaemia; bone differentiation;

(GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX WPI; 2000-572271/53.

XX N-PSDB; AAC58589.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of

KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;
 KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
 XX bone fracture; cartilage damage; artificial joint.
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "signal peptide"
 XX
 XX W09333979-A2.
 XX
 PD 08-JUL-1999.
 XX
 XX 18-DEC-1998; 98WO-US27008.
 XX
 XX 30-DEC-1997; 97US-0068958.
 PR 24-SEP-1998; 98US-0101603.
 PR 30-SEP-1998; 98US-0102540.
 XX
 XX (CHIR) CHIRON CORP.
 PA
 XX Lin H, Cao L;
 XX
 XX WPI; 2000-038344/03.
 DR N-PSDB: AAZ36246.
 XX
 XX New isolated human polynucleotide and secreted proteins can induce
 FT production of other cytokines in certain cell populations -
 XX
 XX Claim 2; Page 113; 120pp; English.
 XX
 CC AY53622-43 represent bone marrow secreted proteins of human bone marrow
 CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or
 CC cell differentiation activity (either inducing or inhibiting). They can
 CC be used to support colony forming cells or factor-dependent cell lines,
 CC to regulate hematopoiesis, and to treat myeloid or lymphoid cell
 CC deficiencies. In addition, they may be used to support the growth and
 CC proliferation of erythroid progenitor cells, and to treat various
 CC anemias. They can have colony stimulating factor (CSF) activity and can
 CC be used to support the growth and proliferation of myeloid cells such as
 CC granulocytes, monocytes or macrophages, to prevent or treat
 CC myelo-suppression, to support the growth and proliferation of
 CC megakaryocytes and platelets, thereby allowing prevention or treatment
 CC of platelet disorders such as thrombocytopenia, to support the growth
 CC and proliferation of hematopoietic stem cells, either in place of or in
 CC conjunction with platelet transfusions, to treat stem cell disorders,
 CC such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to
 CC repopulate the stem cell compartment after irradiation or chemotherapy.
 CC They can be used for growth or differentiation of bone, cartilage,
 CC tendon, ligament, or nerve tissue, as well as for wound healing and
 CC tissue repair and replacement, and in the treatment of burns, incisions
 CC and ulcers, to induce cartilage and/or bone growth in circumstances
 CC where bone is not normally formed and thus have an application in healing
 CC bone fractures and cartilage damage or defects, prophylactic use in
 CC fracture reduction and also in the improved fixation of artificial
 CC joints.
 XX
 XX Sequence 328 AA;
 SQ
 Query Match 100.0%; Score 328; DB 21; Length 328;
 Best Local Similarity 100.0%; Pred. No. 4.9e-295;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMWRPVSLLLLLLRHGAGKSPDAGPHGQGRVHQAPLSDAPHDDAHGQFYDHEAFL 60
 Db 1 MMWRPVSLLLLLLRHGAGKSPDAGPHGQGRVHQAPLSDAPHDDAHGQFYDHEAFL 60
 QY 61 GREVAKFQDLTPESQARLGRIIVDRMDRAGDGVSVLAELRAWTHTQQRHSDVSA 120
 Db 61 GREVAKFQDLTPESQARLGRIIVDRMDRAGDGVSVLAELRAWTHTQQRHSDVSA 120
 QY 121 AWDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180

Db 121 AWDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
 QY 181 SMATREELTAFLLHPEEPFPHMRDIVIAETLDELDRNKDGYVQVEEYIADLYSAEPGEPEPA 240
 Db 181 SMATREELTAFLLHPEEPFPHMRDIVIAETLDELDRNKDGYVQVEEYIADLYSAEPGEPEPA 240
 QY 241 WVQTERQQFRDRLNKGDLGSEVGHVWLPAPADQDPLVEANHLHESDTRDKDGRLSKA 300
 Db 241 WVQTERQQFRDRLNKGDLGSEVGHVWLPAPADQDPLVEANHLHESDTRDKDGRLSKA 300
 QY 301 EILGNWNMFVGSQATNYGEDLTRHDEL 328
 Db 301 EILGNWNMFVGSQATNYGEDLTRHDEL 328
 RESULT 6
 AAU12353
 ID AAU12353 standard; Protein; 328 AA.
 XX AC AAU12353;
 XX DT 24-OCT-2001 (first entry)
 XX DE Human PRO272 polypeptide sequence.
 XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX OS Homo sapiens.
 XX WO200140466-A2.
 XX 07-JUN-2001.
 XX 01-DEC-2000; 2000WO-US32678.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 09-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99US-0170262.
 PR 20-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 30-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 11-FEB-2000; 2000WO-US00376.
 PR 18-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 01-MAR-2000; 2000WO-US05004.
 PR 20-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US07532.
 PR 17-MAY-2000; 2000WO-US08439.
 PR 22-MAY-2000; 2000WO-US13705.
 PR 30-MAY-2000; 2000WO-US14042.
 PR 02-JUN-2000; 2000WO-US14941.
 PR 10-NOV-2000; 2000WO-US15264.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sharwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX

DR WPI; 2001-408281/43.
DR N-PSDB; AAS21425.
XX Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical
XX
XX Claim 12; Fig 364; 813pp; English.
XX
XX AAU12172-AAU12446 represent novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PMNCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIa. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
XX Sequence 328 AA;
SQ

Query Match 100.0%; Score 328; DB 22; Length 328;
Best Local Similarity 100.0%; Pred. No. 4.9e-295;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWRPVSLLLLLLLRHGAQGKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
Db 1 MWRPVSLLLLLLLRHGAQGKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60

Qy 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGVWSLAELRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGVWSLAELRAWIAHTQQRHIRDSVSA 120

Qy 121 AWDYTDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Db 121 AWDYTDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180

Qy 181 SMATREELTAFLHPEEFPHMRDIVIAETLEDLDRNKGQVGVVEEYIADLYSAEPGEEPPA 240
Db 181 SMATREELTAFLHPEEFPHMRDIVIAETLEDLDRNKGQVGVVEEYIADLYSAEPGEEPPA 240

Qy 241 WQTERQQFRDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTRDKGRLSKA 300
Db 241 WQTERQQFRDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTRDKGRLSKA 300

Qy 301 EILGNMNFVGSQATNYGEDLTRHDEL 328
Db 301 EILGNMNFVGSQATNYGEDLTRHDEL 328

RESULT 7
AAG64865
ID AAG64865 standard; protein; 328 AA.
XX
XX AAG64865;
XX
XX 21-SEP-2001 (first entry)
XX Human calcium binding protein.
XX Human; calcium binding protein; HCBP; cell proliferation disorder;
XX

KW cancer.
XX Homo sapiens.
OS
XX US2001012831-A1.
PN
XX 09-AUG-2001.
PD
XX 23-JAN-2001; 2001US-0768840.
PF
XX 21-MAR-1997; 97US-0828212.
PR 07-DEC-1998; 98US-0206499.
PR
XX (INCY-) INCYTE PHARM INC.
PA
XX Hillman JL, Goli SK;
PI
XX WPI; 2001-464391/50.
DR N-PSDB; AAH48279.
DR
XX Human calcium-binding protein, useful in the diagnosis, prevention, and
XX treatment of disorders associated with cell proliferation, e.g.
XX adenocarcinoma, leukemia, lymphoma, melanoma, sarcoma, or
XX teratocarcinoma
PT
XX Claim 1; Fig 1; 30pp; English.
PS
XX The present invention provides the protein and coding sequences of human
XX calcium binding protein (HCBP). The sequences can be used in the
XX diagnosis, prevention and treatment of cell proliferation disorders, such
XX as cancer. The present sequence is the protein of the invention.
XX
XX Sequence 328 AA;
SQ

Query Match 100.0%; Score 328; DB 22; Length 328;
Best Local Similarity 100.0%; Pred. No. 4.9e-295;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWRPVSLLLLLLLRHGAQGKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
Db 1 MWRPVSLLLLLLLRHGAQGKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60

Qy 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGVWSLAELRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGVWSLAELRAWIAHTQQRHIRDSVSA 120

Qy 121 AWDYTDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Db 121 AWDYTDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180

Qy 181 SMATREELTAFLHPEEFPHMRDIVIAETLEDLDRNKGQVGVVEEYIADLYSAEPGEEPPA 240
Db 181 SMATREELTAFLHPEEFPHMRDIVIAETLEDLDRNKGQVGVVEEYIADLYSAEPGEEPPA 240

Qy 241 WQTERQQFRDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTRDKGRLSKA 300
Db 241 WQTERQQFRDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTRDKGRLSKA 300

Qy 301 EILGNMNFVGSQATNYGEDLTRHDEL 328
Db 301 EILGNMNFVGSQATNYGEDLTRHDEL 328

RESULT 8
AAB80250
ID AAB80250 standard; protein; 328 AA.
XX
XX AAB80250;
XX
XX 24-APR-2001 (first entry)
XX Human PRO272 protein.
XX

KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
 KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
 KW antiangiogenic; vasotropic; antiaschmatic; antirheumatic; cancer;
 KW antiarthritic; antifertility; antidiabetic; antiviral; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischaemia; inflammation.

XX Homo sapiens.

XX WO200104311-A1.

XX 18-JAN-2001.

XX 22-FEB-2000; 2000WO-US04414.

XX 07-JUL-1999; 99US-0143048.

XX 26-JUL-1999; 99US-0145698.

XX 28-JUL-1999; 99US-0146222.

XX 08-SEP-1999; 99WO-US20594.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 05-OCT-1999; 99WO-US23089.

XX 29-NOV-1999; 99WO-US28214.

XX 30-NOV-1999; 99WO-US28313.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 20-DEC-1999; 99WO-US30999.

XX 05-JAN-2000; 99WO-US00219.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

XX Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kijavini IJ;

XX Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

XX Williams PM, Wood WI;

XX WPI: 2001-081051/09.

XX N-PSDB; AAF72411.

XX Sixty one nucleic acids encoding PRO polypeptides which are useful in
 the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
 squamous cell carcinoma) and neurodegenerative diseases (e.g.
 Alzheimer's disease) -

XX Claim 1: Fig 80; 393pp; English.

XX The present sequence is one of sixty one novel secreted and

transmembrane PRO polypeptides. The PRO polypeptides are

useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung

squamous cell carcinoma), gastrointestinal disorders (e.g.

enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,

Parkinson's disease), wound repair, cardiovascular disorders (e.g.

endometrial bleeding angiogenesis, ischaemias such as coronary

ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,

rheumatoid arthritis, multiple sclerosis), infertility, AIDS and

diabetes and retinal disorders such as retinitis pigmentosa.

The PRO nucleic acids have applications in molecular biology, including

use as hybridization probes, and in chromosome and gene mapping.

Sequence 328 AA;

Query Match 100.0%; Score 328; DB 22; Length 328;

Best Local Similarity 100.0%; Pred. No. 4.9e-295;

Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPVLVLLLRHGAQKSPDAGPHGQGRVHOAAPLSDAPHDDAHGNFYDHEAPL 60

DB 1 MMWRPVLVLLLRHGAQKSPDAGPHGQGRVHOAAPLSDAPHDDAHGNFYDHEAPL 60

QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAEALRAWIAHTQQRHIDSVA 120

|||||

Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAEALRAWIAHTQQRHIDSVA 120

QY 121 AWDYTDTRDGRGVGHEELRNATYGHYAPGEFHDVEDAETKKMLARDERRFRVADQDGD 180

Db 121 AWDYTDTRDGRGVGHEELRNATYGHYAPGEFHDVEDAETKKMLARDERRFRVADQDGD 180

QY 181 SMATREELTAFLEHPEEPFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEPEA 240

Db 181 SMATREELTAFLEHPEEPFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEPEA 240

QY 241 WQTERQQFRDLNKGDLGSEVGHVWLPAPADQPLVEANHLHESDTDKDRLSKA 300

Db 241 WQTERQQFRDLNKGDLGSEVGHVWLPAPADQPLVEANHLHESDTDKDRLSKA 300

QY 301 EILGNWNNFVGSQATNYGDLTRHDEL 328

Db 301 EILGNWNNFVGSQATNYGDLTRHDEL 328

RESULT 9

AAB53085

ID AAB53085 standard; Protein; 328 AA.

XX AC AAB53085;

XX DT 28-FEB-2001 (first entry)

XX DE Human angiogenesis-associated protein PRO272, SEQ ID NO:113.

XX KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;

cardiac hypertrophy; cardiovascular disorder; endothelial disorder;

angiogenic disorder; atherosclerosis; osteoporosis; hypertension;

myocardial infarction; diabetic retinopathy; rheumatoid arthritis;

Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;

Alzheimer's disease; Huntington's disease; stroke; drug screening;

gene therapy; transgenic animal.

XX OS Homo sapiens.

XX PN WO200053753-A2.

XX PD 14-SEP-2000.

XX PF 05-JAN-2000; 2000WO-US00219.

XX PR 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 05-OCT-1999; 99WO-US23089.

PR 30-NOV-1999; 99WO-US28313.

PR 30-NOV-1999; 99WO-US28409.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

XX (GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;

XX Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;

PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;

XX WPI: 2001-090793/10.

DR N-PSDB; AAC97455.

XX New isolated nucleic acid for producing a PRO polypeptide, analyzing

genetic disorders and treating cardiovascular, endothelial or

PT	angiogenic disorders, such as atherosclerosis, wounds or cancer -	DT	25-MAR-1999 (first entry)	Human secreted protein encoded by gene 46 clone HSJB079.
XX	Claim 69; Fig 44; 293pp; English.	XX		Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX	The invention relates to novel human angiogenesis-associated proteins	KW		diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
CC	designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding	KW		developmental abnormality; foetal deficiency; blood; allergy; renal;
CC	PRO proteins. The invention also relates to vectors and host cells	KW		immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
CC	comprising a PRO nucleic acid, the recombinant production of a PRO	KW		inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
CC	protein, PRO antibodies specific for a PRO protein, fusion proteins	KW		cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
CC	comprising a PRO protein, agonists or antagonists of a PRO protein, and	KW		osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
CC	compounds which inhibit the expression of a PRO gene. The invention	XX		endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
CC	additionally encompasses methods of identifying modulators of PRO	XX		Homo sapiens.
CC	expression or activity; diagnosing a cardiovascular, endothelial or	XX		
CC	angiogenic disorder, or a susceptibility to such a disorder by detecting	XX		
CC	mutations in a PRO gene, or the expression level of a PRO gene within a	XX		
CC	particular tissue; treating a cardiovascular, endothelial or angiogenic	XX		
CC	disorder via the administration of a PRO protein, PRO nucleic acid, or	XX		
CC	PRO agonist or antagonist; a retroviral gene therapy vector comprising a	XX		
CC	PRO nucleic acid; and methods of inhibiting or stimulating endothelial	XX		
CC	cell growth, cardiac hypertrophy or an agonist or antagonist thereof.	XX		
CC	administration of a PRO protein, or an agonist or antagonist thereof.	XX		
CC	PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO	XX		
CC	agonists and PRO antagonists may be used as therapeutic agents to treat	XX		
CC	cardiovascular, endothelial or angiogenic disorders, such as	XX		
CC	atherosclerosis, osteoporosis, myocardial infarction, hypertension,	XX		
CC	diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,	XX		
CC	endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's	XX		
CC	disease, or stroke. PRO nucleic acids are additionally useful in the	XX		
CC	recombinant production of PRO proteins, as hybridisation probes to	XX		
CC	screen libraries to isolate cDNAs with sequence identity to PRO proteins,	XX		
CC	to map genes encoding PRO proteins, to analyse genetic disorders, and in	XX		
CC	gene therapy. PRO nucleic acids can also be used to produce transgenic	XX		
CC	animals useful for the development and screening of potential	XX		
CC	therapeutic agents. The present sequence represents a PRO protein of the	XX		
XX	invention.	XX		
SQ	Sequence 328 AA;	XX		
	Query Match 100.0%; Score 328; DB 22; Length 328;	XX		
	Best Local Similarity 100.0%; Pred. No. 4.9e-295;	XX		
	Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX		
QY	1 MMWRPVLVLLLLLRGAQCKSPDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAPL 60	XX		
DB	1 MMWRPVLVLLLLLRGAQCKSPDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAPL 60	XX		
QY	61 GREVAKFEDLTPEESQARLGRIVDRMDRAGDGDGVVSLAELRAWTIAHTQQRHSDVSA 120	XX		
DB	61 GREVAKFEDLTPEESQARLGRIVDRMDRAGDGDGVVSLAELRAWTIAHTQQRHSDVSA 120	XX		
QY	121 AWDYDFDRGRVGEELRNATYGHYAPGEFHDVEDAETYYKKMLARDERRFRVADQGD 180	XX		
DB	121 AWDYDFDRGRVGEELRNATYGHYAPGEFHDVEDAETYYKKMLARDERRFRVADQGD 180	XX		
QY	181 SMATREELTAFLHPEEPHMRDIVIAETLLEDRNKDGYVVEEYADLYSAEPGEEPA 240	XX		
DB	181 SMATREELTAFLHPEEPHMRDIVIAETLLEDRNKDGYVVEEYADLYSAEPGEEPA 240	XX		
QY	241 WVQTERQOQFRDLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTRDKDGRLSKA 300	XX		
DB	241 WVQTERQOQFRDLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTRDKDGRLSKA 300	XX		
QY	301 EILGNWNMFVGSQATNYGEDLTRHDEL 328	XX		
DB	301 EILGNWNMFVGSQATNYGEDLTRHDEL 328	XX		
RESULT 10		XX		
AAW67852		XX		
ID	AAW67852 standard; Protein: 328 AA.	XX		
XX		XX		
AC	AAW67852;	XX		
XX		XX		

DT	25-MAR-1999 (first entry)	Human secreted protein encoded by gene 46 clone HSJB079.
XX		Human; secreted protein; fusion protein; gene therapy; protein therapy;
DE		diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX		developmental abnormality; foetal deficiency; blood; allergy; renal;
KW		immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW		inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW		cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW		osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX		endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS		Homo sapiens.
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 300	/label= unknown
FT	Misc-difference 328	/label= unknown
FT	Misc-difference 328	/label= unknown
XX	W09842738-A1.	
XX	01-OCT-1998.	
XX	19-MAR-1998;	98WO-US05311.
XX	30-MAY-1997;	97US-0050937.
XX	21-MAR-1997;	97US-0041276.
XX	21-MAR-1997;	97US-0041277.
XX	21-MAR-1997;	97US-0041281.
XX	21-MAR-1997;	97US-0042344.
XX	30-MAY-1997;	97US-0048069.
XX	30-MAY-1997;	97US-0048094.
XX	30-MAY-1997;	97US-0048095.
XX	30-MAY-1997;	97US-0048096.
XX	30-MAY-1997;	97US-0048099.
XX	30-MAY-1997;	97US-0048131.
XX	30-MAY-1997;	97US-0048135.
XX	30-MAY-1997;	97US-0048134.
XX	30-MAY-1997;	97US-0048160.
XX	30-MAY-1997;	97US-0048186.
XX	30-MAY-1997;	97US-0048187.
XX	30-MAY-1997;	97US-0048188.
XX	30-MAY-1997;	97US-0048350.
XX	30-MAY-1997;	97US-0048351.
XX	30-MAY-1997;	97US-0048352.
XX	30-MAY-1997;	97US-0048355.
XX	05-AUG-1997;	97US-0054804.
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX	Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;	
PI	Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;	
PI	Rosen CA, Ruben SM, Shi Y, Young P;	
XX	WPI: 1999-070066/06.	
DR	N-PSDB; AAX00656.	
XX	New isolated human genes and the secreted polypeptides they encode -	
PT	useful for diagnosis and treatment of e.g. cancers, neurological	
PT	disorders, immune diseases, inflammation or blood disorders	
XX	Claim 11; Page 297-298; 385pp; English.	
XX	This sequence represents a secreted human protein encoded by the gene	
CC	clone detailed in the descriptor line. The gene can be used to generate	
CC	fusion proteins by linking to the gene to a human immunoglobulin Fc	
CC	portion (e.g. AAX00602) for increasing the stability of the fused	
CC	protein as compared to the human protein only.	
CC	The invention relates to 87 novel genes and their fragments (nucleic	
CC	acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)	
CC	which are useful for preventing, treating or ameliorating medical	

CC conditions e.g. by protein or gene therapy. Also, pathological
CC polypeptides can be diagnosed by determining the amount of the new
CC the new polynucleotides. Specific uses are described for mutations in
CC polynucleotides, based on which tissues they are most highly expressed in
XX (see AAX00611 for described uses).

SQ Sequence 328 AA;

Query Match 91.28; Score 299; DB 20; Length 328;

Best Local Similarity 100.0%; Pred. No. 3.3e-268;

Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MWPSVLLLLLLRHGAGKPSDPAGPHGGRVHQARPLSDAPHDHAGNFQYDHEAFLG 61

Db 1 MWPSVLLLLLLRHGAGKPSDPAGPHGGRVHQARPLSDAPHDHAGNFQYDHEAFLG 60

QY 62 REVAKFDQLTPEESQARLGRIIVDRMDRAGDGDGWSLAELRAWIAHTQORHIRDSVSA 121

Db 61 REVAKFDQLTPEESQARLGRIIVDRMDRAGDGDGWSLAELRAWIAHTQORHIRDSVSA 120

QY 122 WDVTDRDGRVGEELRNATYGHYAPGEFHDVEAETKKMLARDERRFRVADQDGS 181

Db 121 WDVTDRDGRVGEELRNATYGHYAPGEFHDVEAETKKMLARDERRFRVADQDGS 180

QY 182 MATREELTALHPPEEPPHNRDVIETLEDLRNKDGYVQVEEYIADLYSAEPGEEPAW 241

Db 181 MATREELTALHPPEEPPHNRDVIETLEDLRNKDGYVQVEEYIADLYSAEPGEEPAW 240

QY 242 VOTERQFRDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGLSKA 300

Db 241 VOTERQFRDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGLSKA 299

RESULT 11

AAU87402

ID AAU87402 standard; Protein; 343 AA.

AC AAU87402;

DT 05-JUN-2002 (first entry)

DE Novel central nervous system protein #312.

KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischemia; angiodysplasia;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.

OS Homo sapiens.

XX WO200155318-A2.

PN 02-AUG-2001.

PD 17-JAN-2001; 2001WO-US01332.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205513.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
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PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
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PR 14-AUG-2000; 2000US-0225279.
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PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
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PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 25-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 02-OCT-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
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PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
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PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.

Tue May 20 14:43:20 2003

20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
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PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
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PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 06-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-581633/65.
XX N-PSDB; ABR43732.
XX New isolated nucleic acid encoding a protein for diagnosing,
XX preventing, treating or ameliorating medical conditions and used as
XX food additives or preservatives -
XX Claim 9; SEQ ID NO 920; 837pp; English.
XX The invention describes an isolated nucleic acid molecule (I) encoding a
XX novel central nervous system protein. (I) and polypeptides (III) encoded
XX by (I), are used to treat a medical conditions and in diagnosis of a
XX pathological condition. Disorders which are diagnosed or treated include
XX autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
XX disorders e.g. neoplasms of the breast or liver, cardiovascular disorders

CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukaemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infarction. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
Query Match 75.9%; Score 249; DB 22; Length 343;
Best Local Similarity 100.0%; Pred. No. 6.2e-222;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMWRPSVILLILLRRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDHAGNFQDHEAFL 60
Db 16 MMWRPSVILLILLRRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDHAGNFQDHEAFL 75
QY 61 GREVAKREFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWTATQQRHIRDSVSA 120
Db 76 GREVAKREFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWTATQQRHIRDSVSA 135
QY 121 AWDTYDTRDGRVWELRNATYGHVAPGEEFHDVEDAETFKKMLARDERRFRVADQDGD 180
Db 136 AWDTYDTRDGRVWELRNATYGHVAPGEEFHDVEDAETFKKMLARDERRFRVADQDGD 195
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGVOVEEYIADLYSAEPGEEPA 240
Db 196 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGVOVEEYIADLYSAEPGEEPA 255
QY 241 WQTERQOF 249
Db 256 WQTERQOF 264
RESULT 12
AAM43584
ID AAM43584 standard; Protein; 343 AA.
XX AAM43584;
XX AC AAM43584;
XX DT 22-OCT-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 262.
XX KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antitumor; vulnery; anticonvulsant; antibacterial;
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX OS Homo sapiens.
XX PN WO200155308-A2.
XX XX 02-AUG-2001.
XX PD 17-JAN-2001; 2001WO-US01309.
XX PF 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
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PR 14-AUG-2000; 2000US-0225268.
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PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
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PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226581.
PR 22-AUG-2000; 2000US-0226581.
PR 22-AUG-2000; 2000US-0226588.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235834.
PR 29-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.

PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
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PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-488781/53.

N-PSDB; AAI63890.

New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders -

Claim 11; SEQ ID NO 262; 664pp + Sequence Listing; English.

The invention relates to human polynucleotides (AAI63803-AAI64012) and

the encoded proteins (AA0434497-AA043660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query Match 75.9%; Score 249; DB 22; Length 343;
Best Local Similarity 100.0%; Pred. No. 6.2e-222;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MMWRPSVLLILLRRGAGKPSDPAGPHGGRVHQAAPLSDAPHDDAHGNFYDHEAFL	60
Db	16	MMWRPSVLLILLRRGAGKPSDPAGPHGGRVHQAAPLSDAPHDDAHGNFYDHEAFL	75
QY	61	GREVAKEFDLTPEESQARLGRIVDRMDRAGDGVSLAEALRWIAHQHHRDVSVA	120
Db	76	GREVAKEFDLTPEESQARLGRIVDRMDRAGDGVSLAEALRWIAHQHHRDVSVA	135
QY	121	ANDTDTDRDGRVGEELRNATYHYAPGEEPHDVEDATYKKMLARDERRFRVADQGD	180
Db	136	ANDTDTDRDGRVGEELRNATYHYAPGEEPHDVEDATYKKMLARDERRFRVADQGD	195
QY	181	SNATRELTAFLLHPEEPHMRDIVIAETLEDLRNKGIVQVEEYIADLYSAEPGEEPPA	240
Db	196	SNATRELTAFLLHPEEPHMRDIVIAETLEDLRNKGIVQVEEYIADLYSAEPGEEPPA	255
QY	241	WVQTERQQF 249	
Db	256	WVQTERQQF 264	
RESULT 13			
AAU19946			
ID	AAU19946 standard; Protein; 343 AA.		
XX			
AC	AAU19946;		
XX			
DT	04-DEC-2001 (first entry)		
XX			
DE	Novel human calcium-binding protein #55.		
XX			
KW	Human; calcium-binding protein; calcium flux; neurological disease;		
KW	immune dysfunction; digestive disorder; neoplastic disease;		
KW	blood disorder; infectious disease; gene therapy; immunosuppressive;		
KW	antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;		
KW	virucide.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200155304-A2.		
XX			
PD	02-AUG-2001.		
XX			
PF	17-JAN-2001; 2001WO-US01302.		
XX			
XX	31-JAN-2000; 2000US-0179065.		
PR	04-FEB-2000; 2000US-0180628.		
PR	24-FEB-2000; 2000US-0184564.		
PR	02-MAR-2000; 2000US-0186350.		

PR	16-MAR-2000;	2000US-0189874.
PR	17-MAR-2000;	2000US-0190076.
PR	18-APR-2000;	2000US-0198123.
PR	19-MAY-2000;	2000US-0205515.
PR	07-JUN-2000;	2000US-0209467.
PR	28-JUN-2000;	2000US-0214886.
PR	30-JUN-2000;	2000US-0215135.
PR	07-JUL-2000;	2000US-0216647.
PR	07-JUL-2000;	2000US-0216880.
PR	11-JUL-2000;	2000US-0217487.
PR	11-JUL-2000;	2000US-0217496.
PR	14-JUL-2000;	2000US-0218290.
PR	26-JUL-2000;	2000US-0220963.
PR	26-JUL-2000;	2000US-0220964.
PR	14-AUG-2000;	2000US-0224518.
PR	14-AUG-2000;	2000US-0224519.
PR	14-AUG-2000;	2000US-0225213.
PR	14-AUG-2000;	2000US-0225214.
PR	14-AUG-2000;	2000US-0225266.
PR	14-AUG-2000;	2000US-0225267.
PR	14-AUG-2000;	2000US-0225268.
PR	14-AUG-2000;	2000US-0225270.
PR	14-AUG-2000;	2000US-0225447.
PR	14-AUG-2000;	2000US-0225757.
PR	14-AUG-2000;	2000US-0225758.
PR	14-AUG-2000;	2000US-0225759.
PR	18-AUG-2000;	2000US-0226279.
PR	22-AUG-2000;	2000US-0226681.
PR	22-AUG-2000;	2000US-0226868.
PR	22-AUG-2000;	2000US-0227182.
PR	23-AUG-2000;	2000US-0227009.
PR	30-AUG-2000;	2000US-0228924.
PR	01-SEP-2000;	2000US-0229287.
PR	01-SEP-2000;	2000US-0229343.
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PR	05-SEP-2000;	2000US-0229509.
PR	05-SEP-2000;	2000US-0229513.
PR	06-SEP-2000;	2000US-0230437.
PR	06-SEP-2000;	2000US-0230438.
PR	08-SEP-2000;	2000US-0231242.
PR	08-SEP-2000;	2000US-0231243.
PR	08-SEP-2000;	2000US-0231244.
PR	08-SEP-2000;	2000US-0231413.
PR	08-SEP-2000;	2000US-0231414.
PR	08-SEP-2000;	2000US-0232080.
PR	12-SEP-2000;	2000US-0232081.
PR	14-SEP-2000;	2000US-0231968.
PR	14-SEP-2000;	2000US-0232397.
PR	14-SEP-2000;	2000US-0232398.
PR	14-SEP-2000;	2000US-0232399.
PR	14-SEP-2000;	2000US-0232400.
PR	14-SEP-2000;	2000US-0232401.
PR	14-SEP-2000;	2000US-0233063.
PR	14-SEP-2000;	2000US-0233064.
PR	14-SEP-2000;	2000US-0233065.
PR	21-SEP-2000;	2000US-0234223.
PR	21-SEP-2000;	2000US-0234274.
PR	25-SEP-2000;	2000US-0234997.
PR	25-SEP-2000;	2000US-0234998.
PR	26-SEP-2000;	2000US-0235484.
PR	27-SEP-2000;	2000US-0235834.
PR	27-SEP-2000;	2000US-0235836.
PR	29-SEP-2000;	2000US-0236327.
PR	29-SEP-2000;	2000US-0236367.
PR	29-SEP-2000;	2000US-0236368.
PR	29-SEP-2000;	2000US-0236369.
PR	02-OCT-2000;	2000US-0236370.
PR	02-OCT-2000;	2000US-0236802.
PR	02-OCT-2000;	2000US-0237037.
PR	02-OCT-2000;	2000US-0237038.
PR	02-OCT-2000;	2000US-0237039.
PR	02-OCT-2000;	2000US-0237040.

PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 01-NOV-2000; 2000US-0241826.
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 PR 08-NOV-2000; 2000US-0245474.
 PR 08-NOV-2000; 2000US-0245475.
 PR 08-NOV-2000; 2000US-0245476.
 PR 08-NOV-2000; 2000US-0245477.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
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 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 05-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0256719.
 PR 08-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2000US-0254097.
 PR 05-JAN-2001; 2000US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 DR WPI: 2001-465568/50.
 XX N-PSDB; AAS31631.
 DR Isolated nucleic acid molecule encoding a calcium-binding protein is
 PT used in preventing, treating or ameliorating a medical condition.
 XX
 PS Claim 11; SEQ ID No 143; 542pp; English.
 XX
 XX The present invention relates to the isolation of novel human

CC calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic
 CC sequences encoding for these proteins. The sequences of the invention
 CC are useful in the diagnosis, prevention and/or prognosis of diseases
 CC associated with aberrant calcium flux. Such disorders include
 CC neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
 CC immune dysfunction (e.g. severe combined immunodeficiency, SCID),
 CC digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
 CC disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
 CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
 CC novel calcium-binding proteins are also useful as screening tools to
 CC identify antagonists and/or agonists that may enhance or inhibit
 CC activities mediated by calcium-binding proteins. The polynucleotides of
 CC the invention are also useful in gene therapy. AAU19892-AAU19969
 CC represent the novel human calcium-binding proteins.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 343 AA;

Query Match 75.9%; Score 249; DB 22; Length 343;
 Best Local Similarity 100.0%; Pred. No. 6.2e-222;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLRHGAQCKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
 DB 16 MMWRPSVLLLLLLRHGAQCKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 75
 QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGHWYLAELRAWTAHTQQRHIRDSVSA 120
 DB 76 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGHWYLAELRAWTAHTQQRHIRDSVSA 135
 QY 121 AWDYTDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQDGD 180
 DB 136 AWDYTDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQDGD 195
 QY 181 SMATREELTAFLHPEEFPHMRDIVIAETLEDLRNKGQYVQVEEYIADLYSAEPGEEPPA 240
 DB 196 SMATREELTAFLHPEEFPHMRDIVIAETLEDLRNKGQYVQVEEYIADLYSAEPGEEPPA 255
 QY 241 WYQTERQQF 249
 DB 256 WYQTERQQF 264

RESULT 14
 AAG75587

ID AAG75587 standard; Protein; 240 AA.

XX AC AAG75587;

XX DT 03-SEP-2001 (first entry)

XX DE Human colon cancer antigen protein SEQ ID NO:6351.

XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma.

XX OS Homo sapiens.

XX PN WO200122920-A2.

XX PD 05-APR-2001.

XX PF 28-SEP-2000; 2000WO-US26524.

XX PR 29-SEP-1999; 99US-0157137.

XX PR 03-NOV-1999; 99US-0163280.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;

XX

Db 1 MWRPSVLLLLLLLLLHCAQKSPDAGPHGQGRVHQAAFLSDAPHDDAHGNFQYDHEAFLG 60
QY 62 REVAKFDFDOLTPESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 121
Db 61 REVAKFDFDOLTPESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 121
QY 122 WDTYDTRDGRVGVWEELRN 140
Db 121 WDTYDTRDGRVGVWEELRN 139

Search completed: May 14, 2003, 10:48:38
Job time : 40 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:47:23 ; Search time 20 Seconds
(without alignments)
1576.605 Million cell updates/sec

Title: US-09-768-840-1

Perfect score: 328

Sequence: 1 MWRPSVLLLLLLLRHGAQG.....FVGSQATNYGDLTRHDEL 328

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_73.*

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	5.5	325	2 A45337	reticulocalbin pre
2	18	5.5	331	2 JC4173	reticulocalbin pre
3	9	2.7	402	1 BORUS	sex steroid-bindin
4	8	2.4	90	1 BCHUY	calcyclin - human
5	8	2.4	133	2 S57038	probable membrane
6	8	2.4	147	2 A53180	ribonuclease PL3 (
7	8	2.4	171	2 S19502	hypothetical prote
8	8	2.4	185	2 A49957	CD45-associated 30
9	8	2.4	197	2 S51372	membrane protein L
10	8	2.4	205	2 T48294	pathogenesis relat
11	8	2.4	206	2 A55412	lymphocyte phospho
12	8	2.4	209	1 A26166	Ig lambda-5 chain
13	8	2.4	263	2 S57346	interleukin 15 rec
14	8	2.4	271	2 A48826	low choriolytic ha
15	8	2.4	351	2 S20078	NOV protein - chic
16	8	2.4	356	2 S39605	class I histocompa
17	8	2.4	365	2 S66466	cathepsin E (EC 3.
18	8	2.4	376	2 T03988	Myb-like transcrip
19	8	2.4	381	2 S48049	cholecystokinin B
20	8	2.4	398	2 S66465	cathepsin E (EC 3.
21	8	2.4	399	1 A39697	maize myb-related
22	8	2.4	420	2 I51667	thrombin receptor
23	8	2.4	441	2 F71425	hypothetical prote
24	8	2.4	447	2 A47430	gastrin/cholecysto
25	8	2.4	452	2 A46195	cholecystokinin B
26	8	2.4	452	2 JC2459	gastrin/cholecysto
27	8	2.4	453	2 S32817	hypothetical prote
28	8	2.4	481	2 T22406	gastrin receptor -
29	8	2.4	491	2 A82053	DamX-related prote

30 8 2.4 732 1 LJCHCB
31 8 2.4 754 2 D70536
32 8 2.4 858 1 JC2481
33 8 2.4 976 1 TVMSMD
34 8 2.4 978 2 S16385
35 8 2.4 1302 2 AC2574
36 8 2.4 1309 1 S35484
37 8 2.4 1791 2 T02345
38 8 2.4 1894 2 JC4980
39 7 2.1 35 4 S41911
40 7 2.1 52 2 S05488
41 7 2.1 53 2 S05486
42 7 2.1 57 2 I49627
43 7 2.1 61 1 DNPVBF
44 7 2.1 77 2 A03982
45 7 2.1 82 2 JQ1181

ALIGNMENTS

RESULT 1

A45337

reticulocalbin precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002

C:Accession: A45337; I55203

R:Ozawa, M.; Muramatsu, T.

J. Biol. Chem. 268, 699-705, 1993

A:Title: Reticulocalbin, a novel endoplasmic reticulum resident Ca(2+)-binding protei

A:Reference number: A45337; MUID:93107083; PMID:8416973

A:Contents: teratocarcinoma OTT6050

A:Accession: A45337

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-325 <OZA>

A:Cross-references: GB:D13003; NID:9220581; PIDN:BAA02366.1; PID:d1002865; PID:g22058

A:Note: sequence extracted from NCBI backbone (NCBIP:121512)

R:Ozawa, M.

J. Biochem. 118, 154-160, 1995

A:Title: Structure of the gene encoding mouse reticulocalbin, a novel endoplasmic ret

A:Reference number: I55203; MUID:96015163; PMID:8537305

A:Accession: I55203

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-325 <RES>

A:Cross-references: GB:D43956; NID:g2190295; PIDN:BAA07896.1; PID:g968894

C:Genetics:

A:Introns: 79/2; 144/1; 203/3; 224/1; 290/3

C:Superfamily: reticulocalbin; calmodulin repeat homology

C:Keywords: EF hand

F:1-23/Domain: signal sequence #status predicted <SIG>

F:322-325/Region: endoplasmic reticulum retention signal

Query Match

Best Local Similarity 5.5%; Score 18; DB 2; Length 325;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 305 NNNMFVGSQATNYGDLT 322

DB 302 NNNMFVGSQATNYGDLT 319

|||||

RESULT 2

JC4173

reticulocalbin precursor - human

C:Species: Homo sapiens (man)

C:Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 02-Aug-2002

C:Accession: JC4173

R:Ozawa, M.

J. Biochem. 117, 1113-1119, 1995

A:Title: Cloning of a human homologue of mouse reticulocalbin reveals conservation of

FEBS Lett. 220, 129-135, 1987
A:Title: A cDNA coding for human sex hormone binding globulin. Homology to vitamin K-
A:Reference number: S00077; MUID:87276542; PMID:2956126
A:Accession: S00077
A:Molecule type: mRNA
A:Residues: 1-331 <OZA>
A:Cross-references: DDBJ:D42073; NID:g1262328; PIDN:BAA07670.1; PID:dl008252; PID:g12623
C:comment: This protein is a luminal protein of the endoplasmic reticulum, and is a Ca2+
signal for its retention in the endoplasmic reticulum of cells.
C:Genetics:
A:Gene: GDB:RCN; Rcal
A:Cross-references: GDB:6383031
A:Map position: 11p13-11p13
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: calcium binding; calmodulin binding; EF hand; endoplasmic reticulum
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-331/Product: reticulocalbin homolog #status predicted <MAT>
F:79-111/Domain: calmodulin repeat homology <EF1>
F:113-145/Domain: calmodulin repeat homology <EF2>
F:166-198/Domain: calmodulin repeat homology <EF3>
F:203-235/Domain: calmodulin repeat homology <EF4>
F:244-276/Domain: calmodulin repeat homology <EF5>
F:280-312/Domain: calmodulin repeat homology <EF6>
F:328-331/Region: endoplasmic reticulum retention signal
Query Match 5.5%; Score 18; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 305 NNNMFVGSQATNYGDLT 322
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Db 308 NNNMFVGSQATNYGDLT 325
RESULT 3
BOHUS
sex steroid-binding globulin precursor [validated] - human
N:Alternate names: SBP; sex steroid-binding protein; testosterone-estradiol binding glob
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 24-Feb-1994 #text_change 08-Dec-2000
C:Accession: S09606; A41402; A60876; A26339; S00077; S00065; A03253; A60875; A36093
R:Gershagen, S.; Lundwall, A.; Fernlund, P.
Nucleic Acids Res. 17, 9245-9258, 1989
A:Title: Characterization of the human sex hormone binding globulin (SHBG) gene and dem
A:Reference number: S09606; MUID:90067924; PMID:2587256
A:Accession: S09606
A:Molecule type: DNA
A:Residues: 1-402 <GERL>
A:Cross-references: EMBL:X16349; NID:g36442; PIDN:CAA34398.1; PID:g296673
R:Hammond, G.L.; Underhill, D.A.; Rykse, H.M.; Smith, C.L.
Mol. Endocrinol. 3, 1869-1876, 1989
A:Title: The human sex hormone-binding globulin gene contains exons for androgen-binding
A:Reference number: A41402; MUID:90114193; PMID:2608061
A:Accession: A41402
A:Molecule type: DNA
A:Residues: 1-333,'L',335,'S',337-402 <HAMI>
A:Cross-references: GB:M31651; NID:92979502; PIDN:AAC18778.1; PID:g338075
A:Note: the authors translated the codon CTC for residue 334 as Ala and TCC for residue
R:Bardin, C.W.; Gunsalus, G.L.; Musto, N.A.; Cheng, C.Y.; Reventos, J.; Smith, C.; Under
J. Steroid Biochem. 30, 131-139, 1988
A:Title: Corticosteroid binding globulin, testosterone-estradiol binding globulin, and a
A:Reference number: A60876; MUID:88260097; PMID:3386241
A:Accession: A60876
A:Molecule type: mRNA
A:Residues: 'PQ',23-287,'F',289-402 <BAR>
A:Note: the steroid-binding domain assigned by sequencing a fragment photolabelled with
R:Hammond, G.L.; Underhill, D.A.; Smith, C.L.; Goping, I.S.; Harley, M.J.; Musto, N.A.;
FEBS Lett. 215, 100-104, 1987
A:Title: The cDNA-deduced primary structure of human sex hormone-binding globulin and lo
A:Reference number: A26339; MUID:87190990; PMID:3569533
A:Accession: A26339
A:Molecule type: mRNA
A:Residues: 'Q',23-287,'F',289-402 <HAM2>
A:Cross-references: GB:X05403; NID:g36447; PIDN:CAA28987.1; PID:g36448
R:Gershagen, S.; Fernlund, P.; Lundwall, A.

FEBS Lett. 220, 129-135, 1987
A:Title: A cDNA coding for human sex hormone binding globulin. Homology to vitamin K-
A:Reference number: S00077; MUID:87276542; PMID:2956126
A:Accession: S00077
A:Molecule type: mRNA
A:Residues: 1-331 <OZA>
A:Cross-references: EMBL:X05885; NID:g36450; PIDN:CAA29309.1; PID:g1335306
A:Note: part of this sequence was confirmed by protein sequencing
R:Que, B.G.; Petra, P.H.
FEBS Lett. 219, 405-409, 1987
A:Title: Characterization of a cDNA coding for sex steroid-binding protein of human p
A:Reference number: S00065; MUID:87276521; PMID:2956125
A:Accession: S00065
A:Molecule type: mRNA
A:Residues: 121-402 <QUR>
A:Cross-references: GB:X05792; NID:g36416; PIDN:CAA29234.1; PID:g825718
R:Walsh, K.A.; Titani, K.; Takio, K.; Kumar, S.; Hayes, R.; Petra, P.H.
Biochemistry 25, 7584-7590, 1986
A:Title: Amino acid sequence of the sex steroid binding protein of human plasma.
A:Reference number: A03253; MUID:87101042; PMID:3542030
A:Accession: A03253
A:Molecule type: protein
A:Residues: 30-402 <WAL>
R:Petra, P.H.; Kumar, S.; Hayes, R.; Ericsson, L.H.; Titani, K.
J. Steroid Biochem. 24, 45-49, 1986
A:Title: Molecular organization of the sex steroid-binding protein (SBP) of human pla
A:Reference number: A60875; MUID:86201744; PMID:3702428
A:Accession: A60875
A:Molecule type: protein
A:Residues: 192-195;216-219;361-364;389-392 <PET>
R:Khan, M.S.; Hryb, D.J.; Hashim, G.A.; Romas, N.A.; Rosner, W.
J. Biol. Chem. 265, 18362-18365, 1990
A:Title: Delineation and synthesis of the membrane receptor-binding domain of sex hor.
A:Reference number: A36093; MUID:91009329; PMID:2170408
A:Accession: A36093
A:Molecule type: protein
A:Residues: 77-86 <KRA>
A:Note: membrane receptor-binding region assigned by the binding proteolytic fragment
C:Genetics:
A:Gene: GDB:SHBG
A:Cross-references: GDB:125280; OMIM:182205
A:Map position: 17pter-17p12
A:Introns: 37/3; 68/2; 131/3; 185/3; 239/1; 284/3; 354/1
C:Complex: homodimer
C:Superfamily: sex steroid-binding protein; laminin G repeat homology; sex hormone-bi
C:Keywords: alternative splicing; glycoprotein; homodimer; plasma; steroid binding
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-402/Product: (or 31-402 or 33-402) sex hormone-binding globulin #status experime
F:61-391/Domain: sex hormone-binding globulin homology <SHB>
F:71-220/Domain: laminin G repeat homology <LGR>
F:77-86/Region: receptor binding #status experimental
F:325-402/Region: steroid binding #status experimental
F:36/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:193-217,362-390/Disulfide bonds: #status predicted
F:193-217,362-390/Disulfide bonds: #status predicted
F:273/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:380,396/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 2.7%; Score 9; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 LLLLLLLRH 16
|||||
Db 15 LLLLLLLRH 23
RESULT 4
BCHUY
calcyclin - human
N:Alternate names: growth factor-inducible protein 2A9; prolactin receptor-associated
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1988 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999

C;Accession: A28363; A25645; A30356; PC1222
R;Murphy, L.C.; Murphy, L.J.; Tsuyuki, D.; Duckworth, M.L.; Shiu, R.P.C.
J. Biol. Chem. 263, 2397-2401, 1988
A;Title: Cloning and characterization of a cDNA encoding a highly conserved, putative calcium-binding protein
A;Reference number: A2705; MUID:88115387; PMID:2448309
A;Accession: A28363
A;Molecule type: mRNA
A;Residues: 1-90 <CAL>
A;Cross-references: GB:M18981; NID:g179767; PID:AAA51906.1; PID:g179768
R;Calabretta, B.; Battini, R.; Kaczmarek, L.; de Riel, J.K.; Baserga, R.
J. Biol. Chem. 261, 12628-12632, 1986
A;Title: Molecular cloning of the cDNA for a growth factor-inducible gene with strong homology to the protein tyrosine phosphatase
A;Reference number: A25645; MUID:86304442; PMID:3755724
A;Accession: A25645
A;Molecule type: mRNA
A;Residues: 2-90 <CAL>
A;Cross-references: GB:M14300; NID:g183097; PID:AAA35886.1; PID:g183098
A;Experimental source: fibroblasts
R;Gabius, H.J.; Bardosi, A.; Gabius, S.; Hellmann, K.P.; Karas, M.; Kratzin, H.
Biochem. Biophys. Res. Commun. 163, 506-512, 1989
A;Title: Identification of a cell cycle-dependent gene product as a sialic acid-binding protein
A;Reference number: A30356; MUID:89374276; PMID:2775283
A;Accession: A30356
A;Molecule type: protein
A;Residues: 57-63, 'X', '65', 'X', '67-70', 'X', '72-74' <GAB>
A;Note: the amino end of the intact protein is blocked
R;Tonida, Y.; Terasawa, M.; Kobayashi, R.; Hidaka, H.
Biochem. Biophys. Res. Commun. 189, 1310-1316, 1992
A;Title: Calcyclin and calvasculin exist in human platelets.
A;Reference number: PC1222; MUID:93129189; PMID:1482346
A;Accession: PC1222
A;Molecule type: protein
A;Residues: 27-31; 48-87, 'XX' <TON>
A;Experimental source: platelets
C;Comment: This protein is expressed in a cell cycle-specific manner. Not found in the high in cycling cells. It is overproduced in certain acute myeloid leukemias.
C;Comment: Homology of this protein to the S-100 proteins is of interest given the role of S-100 proteins in cell cycle regulation.
C;Comment: This protein binds sialic acid in the presence of calcium.
C;Genetics:
A;Gene: GDB:S100A6; CACY
A;Cross-references: GDB:I19048; OMIM:114110
A;Map position: 1q21-1q21
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; EF hand; growth regulation; mitogen
F:7-4/Domain: calmodulin repeat homology <EF1>
F:48-80/Domain: calmodulin repeat homology <EF2>

Query Match 2.4%; Score 8; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 EDLDRNKD 217
Db 58 EDLDRNKD 65
|||||||

RESULT 5
S57038
Probable membrane protein YJR023C - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein J1470; hypothetical protein YJR83.19
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 19-Apr-2002
C;Accession: S57038; S57041; S55212
R;de Haan, M.; Grivell, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56771
A;Accession: S57038
A;Molecule type: DNA
A;Residues: 1-133 <ZAG>
A;Cross-references: EMBL:249522; NID:g1015659; PID:g1015661
R;Zagalski, M.; Babinska, B.; Gromadka, R.; Migdalski, A.; Rytka, J.; Sulicka, J.; Herberich, B.
submitted to the Protein Sequence Database, September 1995

A;Reference number: S57040
A;Accession: S57041
A;Molecule type: DNA
A;Residues: 1-93 <HUA>
A;Cross-references: EMBL:249522; MIPS:YJR023C
R;de Haan, M.; Smits, P.H.M.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A;Reference number: S55183
A;Accession: S55212
A;Molecule type: DNA
A;Residues: 1-133 <DEH>
A;Cross-references: EMBL:X87611
C;Genetics:
A;Cross-references: SGD:S0003784
A;Map position: 10R
C;Superfamily: Saccharomyces probable membrane protein YJR023C
C;Keywords: transmembrane protein

Query Match 2.4%; Score 8; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLLL 14
Db 9 VLLLLLLLL 16
|||||||

RESULT 6
A53180
ribonuclease PL3 (EC 3.1.1.1) precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 22-Jun-1999
C;Accession: A53180; B33627
R;Vicentini, A.M.; Hemmings, B.A.; Hofsteenge, J.
Protein Sci. 3, 459-466, 1994
A;Title: Residues 36-42 of liver RNase PL3 contribute to its uridine-preferring substrate specificity
A;Reference number: A53180; MUID:94290321; PMID:8019417
A;Accession: A53180
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-147 <VIC>
A;Cross-references: GB:S73478; NID:g688310; PID:AA831159.1; PID:g688311
R;Hofsteenge, J.; Matthies, R.; Stone, S.R.
Biochemistry 28, 9806-9813, 1989
A;Title: Primary structure of a ribonuclease from porcine liver, a new member of the RNase A family
A;Reference number: A33627; MUID:90122868; PMID:2611266
A;Accession: B33627
A;Status: preliminary
A;Molecule type: protein
A;Residues: 29-147 <HOF>
C;Superfamily: pancreatic ribonuclease
C;Keywords: hydrolase
F:40-68,144/Active site: His, Lys, His #status predicted
F:53-109,67-120,85-135,92-99/disulfide bonds: #status predicted

Query Match 2.4%; Score 8; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLLL 14
Db 8 VLLLLLLLL 15
|||||||

RESULT 7
S19502
hypothetical protein YCR087w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-Apr-2002
C;Accession: S19502
R;Dusterhoft, A.; Erdmann, D.; Hegemann, J.; Philippsen, P.; Schweitzer, B.; Spiegelberg, H.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19351

Tue May 20 14:43:21 2003

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A:Accession: S19502
A:Molecule type: DNA
A:Residues: 1-171 <DUS>
A:Cross-references: EMBL:X59720; NID:g1907116; PID:g1907224; GSPDB:GN00003; MIPS:YCR087w
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T48294
A:Gene: MIPS:YCR087w
A:Cross-references: SGD:S0000683
A:Map position: 3R
C:Superfamily: Saccharomyces hypothetical protein YCR087w

Query Match          2.4%; Score 8; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLL 14
    |||||
Db 83 VLLLLLLL 90

RESULT 8
A49957
CD45-associated 30k phosphoprotein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 11-Jan-2000
C:Accession: A49957
R:Okada, A.; Maizel, A.L.; Kitamura, K.; Ohta, T.; Kimura, S.
J. Biol. Chem. 269, 2357-2360, 1994
A:Title: Molecular cloning of the CD45-associated 30-kDa protein.
A:Reference number: A49957; MUID:94131987; PMID:8300558
A:Accession: A49957
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-185 <YAK>
A:Cross-references: NID:g454750; PIDN:AAA57166.1; PID:g454751
C:Superfamily: human lymphocyte phosphatase-associated phosphoprotein
C:Keywords: phosphoprotein
F:2-185/Product: CD45-associated 30k phosphoprotein #status experimental <YAK>

Query Match          2.4%; Score 8; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLL 14
    |||||
Db 25 VLLLLLLL 32

RESULT 9
S51372
membrane protein LSM - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 20-Jun-2000
C:Accession: S51372
R:Shimizu, Y.; Ogawa, H.; Oka, Y.; Mizuno, R.; Sakoda, S.; Kishimoto, T.; Sugiyama, H.
FEBS Lett. 355, 30-34, 1994
A:Title: Isolation of a cDNA clone encoding a novel membrane protein expressed in lymph
A:Reference number: S51372; MUID:95046370; PMID:7957956
A:Accession: S51372
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-197 <SHI>
A:Cross-references: EMBL:D10105; NID:g602769; PIDN:BAA00986.1; PID:g602770
C:Superfamily: human lymphocyte phosphatase-associated phosphoprotein

Query Match          2.4%; Score 8; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLL 14
    |||||
Db 37 VLLLLLLL 44

RESULT 10
T48294
pathogenesis related protein-like - Arabidopsis thaliana
N:Alternate names: protein F9G14.40
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T48294
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.;
ewes, H.W.; Rudd, S.; Iemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24491
A:Accession: T48294
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-205 <BEV>
A:Cross-references: EMBL:AL162973
A:Experimental source: cultivar Columbia; BAC clone F9G14
C:Genetics:
A:Map position: 5
A:Note: F9G14.40

Query Match          2.4%; Score 8; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SVLLLLLL 13
    |||||
Db 16 SVLLLLLL 23

RESULT 11
A55412
lymphocyte phosphatase-associated phosphoprotein - human
C:Species: Homo sapiens (man)
C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 10-Dec-1999
C:Accession: A55412
R:Schraven, B.; Schoenhaut, D.; Bruyns, E.; Koretzky, G.; Eckerskorn, C.; Wallich, R.
J. Biol. Chem. 269, 29102-29111, 1994
A:Title: LPPAP, a novel 32-kDa phosphoprotein that interacts with CD45 in human lympho
A:Reference number: A55412; MUID:95050730; PMID:7961877
A:Accession: A55412
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <SCH>
A:Cross-references: GB:X81422; NID:g577060; PIDN:CAA57182.1; PID:g577061
C:Genetics:
A:Gene: GDB:LPPAP
A:Cross-references: GDB:439030
A:Superfamily: human lymphocyte phosphatase-associated phosphoprotein
C:Keywords: phosphoprotein

Query Match          2.4%; Score 8; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLL 14
    |||||
Db 37 VLLLLLLL 44

RESULT 12
A26166
Ig lambda-5 chain J region precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26166; J10030; A26434
R:Kudo, A.; Sakauchi, N.; Melchers, F.
EMBO J. 6, 103-107, 1987
A:Title: Organization of the murine Ig-related lambda-5 gene transcribed selectively
A:Reference number: A26166; MUID:87218453; PMID:3107979
A:Accession: A26166
A:Molecule type: DNA
A:Residues: 1-209 <KUD>
```


R; Jongstra, J.; Jongstra-Bilen, J.; Tidmarsh, G.F.; Davis, M.M.
Mol. Immunol. 25, 687-693, 1988
A: Title: The in vitro translation product of the murine lambda 5 gene contains a functional protein
A: Reference number: JLO030; MUID:89039915; PMID:2460755
A: Accession: JLO030
A: Molecule type: mRNA
A: Residues: 1-123, 'ANKATL', 130-209 <JON>
A: Experimental source: pre-B cell, cell lines A2-A15
R; Sakaguchi, N.; Melchers, F.
Nature 324, 579-582, 1986
A: Title: Lambda-5, a new light-chain-related locus selectively expressed in pre-B lymphocytes
A: Reference number: A26434; MUID:87065143; PMID:3024017
A: Accession: A26434
A: Molecule type: mRNA
A: Residues: 92-104 <SAK>
A: Cross-references: GB:M30387
C: Comment: See also PIR:B26434.
C: Comment: This protein is the transcript of immunoglobulin lambda light chain-related gene

C: Genetics:
A: Gene: lambda-5
A: Introns: 65/2, 104/1
C: Superfamily: pre-B cell omega light chain; immunoglobulin homology
C: Keywords: heterotetramer; immunoglobulin
F: 1-30/Domain: signal sequence #status predicted <SIG>
F: 31-209/Product: lambda-5 protein #status predicted <MLS>

Query Match 2.4%; Score 8; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLL 14
Db 18 VLLLLLLL 25

RESULT 13
S57346
Interleukin 15 receptor precursor - mouse
C: Species: Mus musculus (house mouse)
C: Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Nov-1999
C: Accession: S57346
R; Giri, J.G.; Kumaki, S.; Ahldeh, M.; Friend, D.J.; Loomis, A.; Shanebeck, K.; DuBose, R.
EMBO J. 14, 3654-3663, 1995
A: Title: Identification and cloning of a novel IL-15 binding protein that is structurally related to the IL-2 receptor
A: Reference number: S57346; MUID:95369237; PMID:7641685
A: Accession: S57346
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-263 <GIR>
A: Cross-references: EMBL:U22339; NID:9951105; PIDN:AAC52240.1; PID:9951106
C: Superfamily: complement factor H repeat homology
C: Keywords: cytokine receptor
F: 36-96/Domain: complement factor H repeat homology <FH2>

Query Match 2.4%; Score 8; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLL 14
Db 16 VLLLLLLL 23

RESULT 14
A48826
low choriolytic hatching proteinase (EC 3.4.24.-) precursor - Japanese medaka
C: Species: Oryzias latipes (Japanese medaka)
C: Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C: Accession: A48826
R; Yasumasu, S.; Yamada, K.; Akasaka, K.; Mitsunaga, K.; Iuchi, I.; Shimada, H.; Yamagami, Y.
Dev. Biol. 153, 250-258, 1992
A: Title: Isolation of cDNAs for LCE and HCE, two constituent proteases of the hatching

A: Reference number: A48826; MUID:93012471; PMID:1397682
A: Accession: A48826
A: Molecule type: mRNA; protein
A: Residues: 1-271 <YAS>
A: Cross-references: GB:M96169; NID:9213505; PIDN:AAA49440.1; PID:9213506
A: Experimental source: orange red variety, embryo
A: Note: sequence extracted from NCBI backbone (NCBIN:114767, NCBI:114768)
A: Note: part of this sequence, including the amino end of the mature protein, was determined
C: Superfamily: astacin; astacin homology
C: Keywords: glycoprotein; hydrolase; metalloproteinase; zinc
F: 1-20/Domain: signal sequence #status predicted <SIG>
F: 21-271/Product: low choriolytic hatching proteinase #status predicted <MAT>
F: 91-271/Domain: astacin homology <AST>
F: 30, 54, 211/Binding site: carbohydrate (Asn) (covalent) #status predicted
F: 172, 176, 182, 228/Binding site: zinc (His, His, Tyr) #status predicted
F: 173/Active site: Glu #status predicted

Query Match 2.4%; Score 8; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SVLLLLLL 13
Db 8 SVLLLLLL 15

RESULT 15
S20078
NOV protein - chicken
C: Species: Gallus gallus (chicken)
C: Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C: Accession: S20078
R; Joliot, V.; Martinier, C.; Dambrine, G.; Plassiat, G.; Brisac, M.; Crochet, J.; P.
Mol. Cell. Biol. 12, 10-21, 1992
A: Title: Proviral rearrangements and overexpression of a new cellular gene (nov) in m
A: Reference number: S20078; MUID:92107157; PMID:1309586
A: Accession: S20078
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-351 <JOL>
A: Cross-references: EMBL:X59284; NID:963702; PIDN:CAA41975.1; PID:963703
C: Genetics:
A: Gene: NOV

Query Match 2.4%; Score 8; DB 2; Length 351;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLL 14
Db 11 VLLLLLLL 18

Search completed: May 14, 2003, 10:50:07
Job time : 22 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:45:38 ; Search time 14 Seconds
(without alignments)
971.731 Million cell updates/sec

Title: US-09-768-840-1

Perfect score: 328

Sequence: 1 MMWRPSVLLLLLRHGAQG.....FVGSQATNYGDLTRHHDEL 328

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	5.5	325	1 RCNL_MOUSE	Q05186 mus musculus
2	18	5.5	331	1 RCNL_HUMAN	Q15293 homo sapien
3	10	3.0	215	1 YA09_HUMAN	Q9y3b3 homo sapien
4	9	2.7	114	1 NPFF_RAT	Q9wva9 rattus norv
5	9	2.7	315	1 CALU_HUMAN	O43852 homo sapien
6	9	2.7	315	1 CALU_MOUSE	O35887 mus musculus
7	9	2.7	402	1 SHBG_HUMAN	P04278 homo sapien
8	8	2.4	90	1 S106_HUMAN	P06703 homo sapien
9	8	2.4	92	1 S106_CHICK	Q98953 gallus gall
10	8	2.4	110	1 GON2_SUNMU	O97686 suncus muri
11	8	2.4	133	1 YJ23_YEAST	P47094 saccharomyc
12	8	2.4	141	1 LSHB_TRIVU	O46482 trichosurus
13	8	2.4	147	1 RNL4_PIG	P15468 sus scrofa
14	8	2.4	171	1 YCX7_YEAST	P25652 saccharomyc
15	8	2.4	197	1 PTCA_MOUSE	Q64897 mus musculus
16	8	2.4	206	1 PTCA_HUMAN	Q14761 homo sapien
17	8	2.4	271	1 LCE_ORYLA	P31579 oryzias lat
18	8	2.4	273	1 SZ16_HUMAN	Q9h2a7 homo sapien
19	8	2.4	346	1 LICH_ACILW	P28686 gallus gall
20	8	2.4	351	1 NOV_CHICK	P42642 coturnix co
21	8	2.4	353	1 NOV_COTJA	Q15049 homo sapien
22	8	2.4	377	1 MLC1_HUMAN	P70269 mus musculus
23	8	2.4	397	1 CATE_MOUSE	P16228 rattus norv
24	8	2.4	398	1 CATE_RAT	P27898 zea mays (m
25	8	2.4	399	1 MYBP_MAIZE	P47749 xenopus lae
26	8	2.4	420	1 PAR1_XENLA	P32239 homo sapien
27	8	2.4	447	1 GASR_HUMAN	P46627 oryctolagus
28	8	2.4	452	1 GASR_RABIT	P30553 rattus norv
29	8	2.4	452	1 GASR_RAT	P30552 canis fami
30	8	2.4	453	1 GASR_CANFA	P79266 bos taurus
31	8	2.4	454	1 GASR_BOVIN	Q02818 homo sapien
32	8	2.4	461	1 NCBI_HUMAN	P78539 homo sapien
33	8	2.4	464	1 SRPX_HUMAN	

34	8	2.4	501	1 PTGI_MOUSE	O35074 mus musculus
35	8	2.4	501	1 PTGI_RAT	Q62969 rattus norv
36	8	2.4	519	1 PPBT_CHICK	Q92058 gallus gall
37	8	2.4	633	1 HS7B_DROME	P11146 drosophila
38	8	2.4	732	1 CADL_CHICK	P33145 gallus gall
39	8	2.4	734	1 PURL_MYCTU	P54876 mycobacteri
40	8	2.4	975	1 KIT_CANFA	O97799 canis fami
41	8	2.4	977	1 KFMS_MOUSE	P09581 mus musculus
42	8	2.4	978	1 KFMS_RAT	Q00495 rattus norv
43	8	2.4	1310	1 ACE_RABIT	P12822 oryctolagus
44	7	2.1	31	1 LPL_BUCRP	Q53017 buchmera ap
45	7	2.1	61	1 DNBI_BFDV	P13893 budgerigar

ALIGNMENTS

RESULT 1

RCNL_MOUSE	ID	RCNL_MOUSE	STANDARD	PRT	325 AA.
AC	Q05186;				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Reticulocalbin 1 precursor.				
GN	RCN1 OR RCN OR RCAL.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93107083; PubMed=8416973;				
RA	Ozawa M., Muramatsu T.;				
RT	"Reticulocalbin, a novel endoplasmic reticulum resident				
RT	Ca(2+)-binding protein with multiple EF-hand motifs and a				
RL	carboxyl-terminal HDEL sequence.";				
RL	J. Biol. Chem. 268:699-705(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=129/SV; TISSUE=Liver;				
RX	MEDLINE=96015163; PubMed=8537305;				
RA	Ozawa M.;				
RT	"Structure of the gene encoding mouse reticulocalbin, a novel				
RT	endoplasmic reticulum-resident Ca(2+)-binding protein with multiple				
RT	EF-hand motifs.";				
RL	J. Biochem. 118:154-160(1995).				
RN	[3]				
RP	SEQUENCE OF 24-39.				
RC	TISSUE=Fibroblast;				
RX	MEDLINE=95009907; PubMed=7523108;				
RA	Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;				
RT	"Separation and sequencing of familial and novel murine proteins				
RT	using preparative two-dimensional gel electrophoresis.";				
RL	Electrophoresis 15:735-745(1994).				
CC	-1- FUNCTION: MAY REGULATE CALCIUM-DEPENDENT ACTIVITIES IN THE				
CC	ENDOPLASMIC RETICULUM LUMEN OR POST-ER COMPARTMENT.				
CC	-1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.				
CC	-1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING				
CC	SITES; POTENTIAL SITES II AND VI HAVE LOST AFFINITY FOR CALCIUM.				
CC	-1- SIMILARITY: BELONGS TO THE CREC FAMILY.				
CC	-1- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.				
CC	-----				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; D13003; BAA02366.1; -.				
DR	EMBL; D43956; BAA07896.1; -.				


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DR EMBL; D43952; BAA07896.1; JOINED.
DR EMBL; D43954; BAA07896.1; JOINED.
DR EMBL; D43955; BAA07896.1; JOINED.
DR PIR; A45337; A45337.
DR MGD; MGI:104559; RGN.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00036; ehand; 6.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00018; EF_HAND; 3.
KW Calcium-binding; Endoplasmic reticulum; Signal; Glycoprotein; Repeat;
KW Repeat.
FT SIGNAL 1 23 RETICULOCALBIN 1.
FT CHAIN 24 325 EF-HAND 1.
FT CA_BIND 86 97 EF-HAND 2 (POSSIBLY ANCESTRAL).
FT CA_BIND 122 133 EF-HAND 3.
FT CA_BIND 173 184 EF-HAND 4.
FT CA_BIND 210 221 EF-HAND 5.
FT CA_BIND 251 262 EF-HAND 6 (POSSIBLY ANCESTRAL).
FT CA_BIND 287 298 PREVENT SECRETION FROM ER.
FT SITE 322 325 K -> G (IN REF. 3).
FT SITE 47 47 N-LINKED (GLCNAC...) (PARTIAL).
FT CONFLICT 24 24 K -> I (IN REF. 3).
FT CONFLICT 34 34 R -> I (IN REF. 3).
FT CONFLICT 37 39 SEL -> DEE (IN REF. 3).
SQ SEQUENCE 325 AA; 38113 MW; 0470B10B5A8BC76D CRC64;

Query Match 5.5%; Score 18; DB 1; Length 325;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 NWNMFVGSQATNYGEDLT 322
DB 302 NWNMFVGSQATNYGEDLT 319
|||||

RESULT 2
RCNL_HUMAN
ID RCNL_HUMAN STANDARD; PRT; 331 AA.
AC Q15293;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Reticulocalbin 1 precursor.
GN RCNL OR RCN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96172582; PubMed=8586628;
RA Ozawa M.;
RT "Cloning of a human homologue of mouse reticulocalbin reveals
RT conservation of structural domains in the novel endoplasmic reticulum
RT resident Ca(2+)-binding protein with multiple EF-hand motifs.";
RL J. Biochem. 117:1113-1119(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX Coville G.;
RA Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RC -!- FUNCTION: MAY REGULATE CALCIUM-DEPENDENT ACTIVITIES IN THE
CC -!- ENDOPLASMIC RETICULUM LUMEN OR POST-ER COMPARTMENT.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES; POTENTIAL SITES II AND VI HAVE LOST AFFINITY FOR CALCIUM
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CREC FAMILY.
CC -!- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.
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EMBL; D42073; BAA07670.1; -.
EMBL; AL078612; CAB53067.1; -.
Genew; HGNC:9934; RCN1.
MIM; 602735;
InterPro; IPR002048; EF-hand.
InterPro; IPR000886; ER_target.
Pfam; PF00036; ehand; 6.
SMART; SM00054; EFh; 3.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Endoplasmic reticulum; Signal; Glycoprotein; Repeat;
KW Polymorphism.
FT SIGNAL 1 29 RETICULOCALBIN 1.
FT CHAIN 30 331 EF-HAND 1 (POTENTIAL).
FT CA_BIND 92 103 EF-HAND 2 (POSSIBLY ANCESTRAL).
FT CA_BIND 128 139 EF-HAND 3 (POTENTIAL).
FT CA_BIND 179 190 EF-HAND 4 (POTENTIAL).
FT CA_BIND 216 227 EF-HAND 5 (POTENTIAL).
FT CA_BIND 257 268 EF-HAND 6 (POSSIBLY ANCESTRAL).
FT CA_BIND 293 304 PREVENT SECRETION FROM ER.
FT SITE 328 331 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 53 53 T -> N (IN DBSNP:1061145).
FT VARIANT 71 71 /FTID-VAR_011964.
FT VARIANT 73 73 D -> Y (IN DBSNP:1804281).
FT VARIANT 74 74 Q -> E (IN DBSNP:1061143).
FT VARIANT 188 188 /FTID-VAR_011966.
FT VARIANT 188 188 R -> P (IN DBSNP:1061080).
FT SEQUENCE 331 AA; 38890 MW; 608AAD536963F789 CRC64;

Query Match 5.5%; Score 18; DB 1; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 NWNMFVGSQATNYGEDLT 322
DB 308 NWNMFVGSQATNYGEDLT 325
|||||

RESULT 3
YA09_HUMAN
ID YA09_HUMAN STANDARD; PRT; 215 AA.
AC Q9Y3B3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein CGI-109 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20272150; PubMed=10810093;
RA Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
RT "Identification of novel human genes evolutionarily conserved in
RT Caenorhabditis elegans by comparative proteomics.";
RL Genome Res. 10:703-713(2000).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Endoplasmic
CC reticulum (By similarity).
CC -!- SIMILARITY: BELONGS TO THE EMP24/GP25L FAMILY.
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DR EMBL: AFI51867; AAD34104.1;
 DR InterPro: IPR000348; Emp24_gp25L_p24.
 DR Pfam: PF01105; EMP24_GP25L; 1.
 KW Hypothetical protein; Transmembrane; Signal;
 KW Endoplasmic reticulum.
 FT SIGNAL 1 23
 FT CHAIN 24 215
 FT DOMAIN 24 176
 FT TRANSMEM 177 199
 FT DOMAIN 200 215
 FT CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 215 AA; 24354 MW; 5C4D5BBE8054857B CRC64;

Query Match 3.0%; Score 10; DB 1; Length 215;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 SVLLLLLLL 15
 DB 10 SVLLLLLLL 19

RESULT 4

NPFF_RAT STANDARD; PRT; 114 AA.
 AC Q9WV9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRamide-related peptides precursor [Contains: Neuropeptide SF
 DE (NPFF); Neuropeptide FF (NPFF); Neuropeptide AF-like (NPAF)].
 GN NPFF.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Brain;
 RX MEDLINE=99238783; PubMed=10220558;
 RA Vilim F.S., Aarnisalo A.A., Nieminen M.L., Lintunen M., Karlstedt K.,
 RA Kontinen V.K., Kalso E., States B., Panula P., Ziff E.;
 RT "Gene for pain modulatory neuropeptide NPFF: induction in spinal cord
 RT by noxious stimuli.";
 RL Mol. Pharmacol. 55:804-811(1999).

CC -1- FUNCTION: MORPHINE MODULATING PEPTIDES. HAVE WIDE-RANGING
 CC PHYSIOLOGIC EFFECTS, INCLUDING THE MODULATION OF MORPHINE-INDUCED
 CC ANALGESIA, ELEVATION OF ARTERIAL BLOOD PRESSURE, AND INCREASED
 CC SOMATOSTATIN SECRETION FROM THE PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.

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DR EMBL: AFI48700; AAD39828.1;
 KW Neuropeptide; Amidation; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21
 FT PROPEP 22 69
 FT PEPTIDE 72 82
 FT PEPTIDE 75 82
 FT PROPEP 85 100
 FT PEPTIDE 101 111
 FT MOD_RES 82
 AMIDATION (G-83 PROVIDE AMIDE GROUP) (BY

FT MOD_RES 111 111
 FT SEQUENCE 114 AA; 13152 MW; 482ABAB7BA28F9E4 CRC64;
 SO SIMILARITY).
 SIMILARITY).
 Query Match 2.7%; Score 9; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 VLLLLLLL 15
 DB 8 VLLLLLLL 16

RESULT 5

CALU_HUMAN STANDARD; PRT; 315 AA.
 ID CALU_HUMAN
 AC Q43852; O60456;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calumenin precursor (IEF SSP 9302).
 GN CALU
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CALCIUM-BINDING DATA.
 RC TISSUE-Keratinocytes;
 RX PubMed=9675259;
 RA Vorum H., Liu X., Madsen P., Rasmussen H.H., Honore B.;
 RT "Molecular cloning of a cDNA encoding human calumenin, expression in
 RT Escherichia coli and analysis of its Ca2+-binding activity.";
 RL Biochim. Biophys. Acta 1386:121-131(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98260687; PubMed=9598325;
 RA Yabe D., Taniwaki M., Nakamura T., Kanazawa N., Tashiro K., Honjo T.;
 RT "Human calumenin gene (CALU): cDNA isolation and chromosomal mapping
 RT to 7q32.";
 RL Genomics 49:331-333(1998).
 RN [3]
 RP SUBCELLULAR LOCATION.
 RX PubMed=10222138;
 RA Vorum H., Hager H., Christensen B.M., Nielsen S., Honore B.;
 RT "Human calumenin localizes to the secretory pathway and is secreted to
 RT the medium.";
 RL Exp. Cell Res. 248:473-481(1999).

CC -1- FUNCTION: NOT KNOWN. BINDS 7 CALCIUM IONS WITH A LOW AFFINITY.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen and secreted.
 CC -1- TISSUE SPECIFICITY: Ubiquitously expressed. Expressed at high
 CC levels in heart, placenta and skeletal muscle, at lower levels in
 CC lung, kidney and pancreas and at very low levels in brain and
 CC liver.

CC -1- SIMILARITY: BELONGS TO THE CREC FAMILY.
 CC -1- SIMILARITY: CONTAINS 7 EF-HAND CALCIUM-BINDING DOMAINS.
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DR EMBL: U67280; AAB97725.1;
 DR EMBL: AF013759; AAC17216.1;
 DR Genew; HGNC:1458; CALU.
 DR MIM; 603420;
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 6.
 DR SMART; SM00054; Efh; 2.

Tue May 20 14:43:21 2003

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DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Endoplasmic reticulum; Signal; Repeat.
FT SIGNAL 1 19
FT CHAIN 20 315
FT CA_BIND 81 92
FT CA_BIND 117 128
FT CA_BIND 164 175
FT CA_BIND 201 212
FT CA_BIND 242 253
FT CA_BIND 278 289
FT CA_BIND 313 315
FT CARBOHYD 131 131
FT SITE 312 315
FT CONFLICT 207 207
FT SEQUENCE 315 AA; 37107 MW; 25BAE5A9B527375 CRC64;

Query Match 2.7%; Score 9; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 FDQLTPES 76
DB 61 FDQLTPES 69

RESULT 6
CALU_MOUSE
ID CALU_MOUSE STANDARD; PRT; 315 AA.
AC 035887;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calumenin precursor.
GN CALU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=ICR; TISSUE=Heart;
RX MEDLINE=97364750; PubMed=9218460;
RA Yabe D., Nakamura T., Kanazawa N., Tashiro K., Honjo T.;
RT "Calumenin, a Ca2+-binding protein retained in the endoplasmic
RL reticulum with a novel carboxyl-terminal sequence, HDEF.";
RL J. Biol. Chem. 272:18232-18239(1997).
CC -!- FUNCTION: NOT KNOWN, BINDS 7 CALCIUM IONS WITH A LOW AFFINITY (BY
CC similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: BELONGS TO THE CREC FAMILY.
CC -!- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
CC EMBL; U81829; AAC53316.1; -.
CC MGD; MGI:1097158; Calu.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 6.
CC SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Endoplasmic reticulum; Signal; Repeat.
FT SIGNAL 1 19
FT CHAIN 20 315
FT CA_BIND 81 92
FT CA_BIND 117 128
FT CA_BIND 164 175
FT CA_BIND 201 212
FT CA_BIND 242 253
FT CA_BIND 278 289
FT CA_BIND 313 315
FT CARBOHYD 131 131
FT SITE 312 315
FT CONFLICT 207 207
FT SEQUENCE 315 AA; 37107 MW; 25BAE5A9B527375 CRC64;

Query Match 2.7%; Score 9; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 FDQLTPES 76
DB 61 FDQLTPES 69

RESULT 7
SHBG_HUMAN
ID SHBG_HUMAN STANDARD; PRT; 402 AA.
AC P04278; Q16616; P14689;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sex hormone-binding globulin precursor (SHBG) (sex steroid-binding
DE protein) (SBP) (testis-specific androgen-binding protein) (ABP).
DE SHBG.
GN SHBG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Testis;
RX MEDLINE=90067924; PubMed=2587256;
RA Gershagen S., Lundwall A., Fernlund P.;
RT "Characterization of the human sex hormone binding globulin (SHBG)
RL gene and demonstration of two transcripts in both liver and testis.";
RL Nucleic Acids Res. 17:9245-9258(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Testis;
RX MEDLINE=90114193; PubMed=2608061;
RA Hammond G.L., Underhill D.A., Rykse H.M., Smith C.L.;
RT "The human sex hormone-binding globulin gene contains exons for
RL androgen-binding protein and two other testicular messenger RNAs.";
RL Mol. Endocrinol. 3:1869-1876(1989).
RN [3]
RP SEQUENCE OF 22-402 FROM N.A. (ISOFORM 1).
RC TISSUE=Liver;
RX MEDLINE=87190990; PubMed=3569533;
RA Hammond G.L., Underhill D.A., Smith C.L., Goping I.S., Harley M.J.;
RT "The cDNA-decoded primary structure of human sex hormone-binding
RL globulin and location of its steroid-binding domain.";
RL FEBS Lett. 215:100-104(1987).
RN [4]
RP SEQUENCE OF 47-402 FROM N.A. (ISOFORM 1).
RC TISSUE=Liver;
RX MEDLINE=87276542; PubMed=2956126;
RA Gershagen S., Fernlund P., Lundwall A.;
RT "A cDNA coding for human sex hormone binding globulin. Homology to
RL vitamin K-dependent protein S.";
RL FEBS Lett. 220:129-135(1987).
RN [5]
RP SEQUENCE OF 121-402 FROM N.A. (ISOFORM 1).
RC TISSUE=Liver;
RX MEDLINE=87276521; PubMed=2956125;
RA Que B.G., Petra P.H.;
RT "Characterization of a cDNA coding for sex steroid-binding protein of
RL human plasma.";
RL FEBS Lett. 219:405-409(1987).
RN [6]
RP SEQUENCE OF 30-54.
RX MEDLINE=86201807; PubMed=3702459;

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RA Hammond G.L., Robinson P.A., Sugino H., Ward D.N., Finne J.;
 RT "Physicochemical characteristics of human sex hormone binding
 RT globulin: evidence for two identical subunits.",
 RL J. Steroid Biochem. 24:815-824(1986).
 RP SEQUENCE OF 30-402.
 RX MEDLINE-87101042; PubMed-3542030;
 RA Walsh K.A., Titani K., Takio K., Kumar S., Hayes R., Petra P.H.;
 RT "Amino acid sequence of the sex steroid binding protein of human
 RT blood plasma.",
 RL Biochemistry 25:7584-7590(1986).
 RN [8]
 RP VARIANT ASN-356, AND CARBOHYDRATE-LINKAGE SITE ASN-356.
 RX MEDLINE-93016620; PubMed-1400872;
 RA Power S.G.A., Bocchinfuso W.P., Pallesen M., Wamels-Rodenhiiser S.,
 RT Van Baelen H., Hammond G.L.;
 RT "Molecular analyses of a human sex hormone-binding globulin variant:
 RT evidence for an additional carbohydrate chain.",
 RL J. Clin. Endocrinol. Metab. 75:1066-1070(1992).
 RN [9]
 RP VARIANT ASN-356.
 RX MEDLINE-95229819; PubMed-7714097;
 RA Hardy D.O., Carino C., Catterall J.F., Larrea F.;
 RT "Molecular characterization of a genetic variant of the steroid
 RT hormone-binding globulin gene in heterozygous subjects.",
 RL J. Clin. Endocrinol. Metab. 80:1253-1256(1995).
 CC [1-] FUNCTION: Functions as an androgen transport protein, but may also
 CC be involved in receptor mediated processes. Each dimer binds one
 CC molecule of steroid. Specific for 5-alpha-dihydrotestosterone,
 CC testosterone, and 17-beta-estradiol. Regulates the plasma
 CC metabolic clearance rate of steroid hormones by controlling their
 CC plasma concentration.
 CC [1-] SUBUNIT: Homodimer.
 CC [1-] SUBCELLULAR LOCATION: Secreted. In testis, it is synthesized by
 CC the Sertoli cells, secreted into the lumen of the seminiferous
 CC tubule and transported to the epididymis (By similarity).
 CC [1-] ALTERNATIVE PRODUCTS: At least 2 isoforms; 1/SHBG/SHBG-1 (shown
 CC here) and 2/sex hormone binding globulin-gene-related protein
 CC (SHBG-2); are produced by alternative splicing.
 CC [1-] TISSUE SPECIFICITY: Isoforms 1 and 2 are present in liver and
 CC testis.
 CC [1-] SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
 CC
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 CC
 CC EMBL; X16349; CAA34398.1; -
 CC EMBL; X16350; CAA34399.1; -
 CC EMBL; X16351; CAA34400.1; -
 CC EMBL; M31651; AAC18778.1; -
 CC EMBL; X05403; CAA28987.1; -
 CC EMBL; X05885; CAA29309.1; -
 CC EMBL; X05792; CAA29234.1; -
 CC PIR; A03253; BOHUS
 CC PIR; A26339; A26339
 CC PIR; A41402; A41402
 CC PIR; S00077; S00077
 CC PIR; S09606; S09606
 CC GlycoSuiteDB; P04278; -
 CC Genew; HGNC:10839; SHBG.
 CC MIM; 182205; -
 CC InterPro; IPR001791; Laminin_G.
 CC Pfam; PF00054; Laminin_G; 1.
 CC SMART; SM00282; Laminin_G; 1.
 CC PROSITE; PS00025; LAM_G_DOMAIN; 1.
 CC Steroid-binding; Glycoprotein; Repeat; Signal; Alternative splicing;
 CC Polymorphism. 1 29
 FT SIGNAL

FT CHAIN 30 402
 FT DOMAIN 45 217
 FT DOMAIN 224 390
 FT DISULFID 193 217
 FT DISULFID 362 390
 FT CARBOHYD 36 36
 FT CARBOHYD 356 356
 FT CARBOHYD 380 380
 FT CARBOHYD 396 396
 FT VARSPLIC 1 37
 FT VARSPLIC 285 293
 FT VARSPLIC 294 402
 FT VARIANT 356 356
 FT CONFLICT 22 22
 FT CONFLICT 47 55
 FT CONFLICT 334 334
 FT CONFLICT 336 336
 SQ SEQUENCE 402 AA; 43779 MW; 5A3B1885E4E7A460 CRC64;
 Query Match 2.7%; Score 9; DB 1; Length 402;
 Best Local Similarity 100.0%; Pred. No. 0.85;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 8 LLLLLLLH 16
 Db 15 LLLLLLLH 23
 RESULT 8
 ID S106_HUMAN STANDARD; PRT; 90 AA.
 AC P06703;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JUN-1988 (Rel. 06, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcyclin (Prolactin receptor associated protein) (PRA) (Growth
 DE factor-inducible protein 2A9) (S100 calcium-binding protein A6)
 DE (MLN 4).
 GN S100A6 OR CACY.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88115387; PubMed-2448309;
 RA Murphy L.C., Murphy L.J., Tsuyuki D., Duckworth M.L., Shiu R.P.C.;
 RT "Cloning and characterization of a cDNA encoding a highly conserved,
 RT putative calcium binding protein, identified by an anti-prolactin
 RT receptor antiserum.",
 RL J. Biol. Chem. 263:2397-2401(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Fibroblast;
 RX MEDLINE-86304442; PubMed-3755724;
 RA Calabretta B., Battini R., Kaczmarek L., de Riel J.K., Baserga R.;
 RT "Molecular cloning of the cDNA for a growth factor-inducible gene
 RT with strong homology to S-100, a calcium-binding protein.",
 RL J. Biol. Chem. 261:12628-12632(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87250432; PubMed-3036810;
 RA Ferrari S., Calabretta B., Deriel J.K., Battini R., Chezzo F.,
 RA Lauret E., Griffin C., Emanuel B.S., Gurrieri F., Baserga R.;
 RT "Structural and functional analysis of a growth-regulated gene, the
 RT human calcyclin.",
 RL J. Biol. Chem. 262:8325-8332(1987).
 RN [4]

SEX HORMONE-BINDING GLOBULIN.
 LAMININ G-LIKE 1.
 LAMININ G-LIKE 2.

O-LINKED.
 /FTID-CAR_000174.
 N-LINKED (GLCNAC. .) (IN VARIANT ASN-
 356).
 N-LINKED (GLCNAC. .).
 MESRGPLATSLRLLLLRHTRGWLRLPLPTQ -->
 PRFGSPAVLFKLVAVITCSLRLTHPRPW (IN
 ISOFORM 2).
 KVLSSSGS --> EKTLPPLPA (IN ISOFORM 2).
 MISSING (IN ISOFORM 2).
 D --> N.
 /FTID-VAR_013129.
 R --> Q (IN REF. 3).
 LNSGPGQEP --> VHSAAQTTL (IN REF. 4).
 A --> L (IN REF. 2).
 L --> S (IN REF. 2).

RESULT 15	
PTCA_MOUSE	STANDARD;
ID PTCA_MOUSE	
AC Q64697;	
DT 15-JUN-2002 (Rel. 41, Created)	PRT; 197 AA.

DR PIR: B330267; RNaseA; 1.
DR HSSP: P34096; 1RNF.
DR GlycoSuiteDB: PL5468; -.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaase; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.


```

DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein tyrosine phosphatase receptor type C-associated protein
DE (PTPRC-associated protein) (CD45-associated protein) (CD45-AP) (LSM-
DE 1).
GN PTPRCAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Lymphoid;
RX MEDLINE=95046370; PubMed=7957956;
RA Shimizu Y., Ogawa H., Oka Y., Mizuno R., Sakoda S., Kishimoto T.,
RA Sugiyama H.;
RT "Isolation of a cDNA clone encoding a novel membrane protein expressed
RT in lymphocytes.";
RL FEBS Lett. 355:30-34(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Blood;
RX MEDLINE=94131987; PubMed=8300558;
RA Takeda A., Maizel A.L., Kitamura K., Ohta T., Kimura S.;
RT "Molecular cloning of the CD45-associated 30-kDa protein.";
RL J. Biol. Chem. 269:2357-2360(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
CC -|- SUBUNIT: Interacts with CD45/PTPRC.
CC -|- PTM: Phosphorylated on tyrosine residues.
CC -|- TISSUE SPECIFICITY: Leukocyte-specific. Expressed in B- and T-cell
CC lines, in spleen, thymus, and bone marrow of adult mice, and in
CC embryos.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D10105; BAA00986.1;
DR EMBL; U03856; AAA67166.1; ALT_INIT.
DR EMBL; BC013273; AAH13273.1; -.
DR MGD; MGI:97811; Ptpcap.
KW Transmembrane; Phosphorylation.
FT TRANSMEM 33 53 POTENTIAL.
FT CONFLICT 55 55 R -> C (IN REF. 2).
SQ SEQUENCE 197 AA; 20370 MW; B313F88693F084AA CRC64;
Query Match
Best Local Similarity 2.4%; Score 8; DB 1; Length 197;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 7 VLLLLLLL 14
Db 37 VLLLLLLL 44

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Search completed: May 14, 2003, 10:48:59
Job time : 16 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:46:38 ; Search time 34 Seconds
(without alignments)
1987.749 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 328
Sequence: 1 MMWRPSVLLLLLRHGAQG.....FVGSQATWNGEDLTHHDEL 328

Scoring table: OLIGO
Gapop 60.0 , Capext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	328	100.0	328	4	Q96D15	Q96d15 homo sapien
2	235	71.6	328	4	Q9HBZ8	Q9hbz8 homo sapien
3	57	17.4	259	11	Q9CTD4	Q9ctd4 mus musculus
4	57	17.4	315	11	Q99K35	Q99k35 mus musculus
5	25	7.6	328	11	Q9R137	Q9r137 mus musculus
6	25	7.6	98	11	Q93399	Q93399 rattus norv
7	19	5.8	322	13	Q93434	Q93434 figu rubrip
8	10	3.0	217	4	Q9Y3Q3	Q9y3q3 homo sapien
9	9	2.7	269	12	Q9VAZ4	Q9vaz4 white spot
10	9	2.7	296	4	Q9NR43	Q9nr43 homo sapien
11	9	2.7	296	6	Q9WZ46	Q9wz46 sus scrofa
12	9	2.7	315	4	Q96RL3	Q96rl3 homo sapien
13	8	2.4	26	11	Q9ESQ6	Q9esc6 mus musculus
14	8	2.4	58	11	Q9JHQ7	Q9jhg7 mus musculus
15	8	2.4	62	5	Q9NLY0	Q9nly0 leishmania
16	8	2.4	70	5	Q9VUT7	Q9vut7 drosophila

17	8	2.4	100	5	Q9W4Q5	Q9w4q5 drosophila
18	8	2.4	100	10	Q9LDB6	Q9ldg6 oryza sativ
19	8	2.4	115	12	Q9L7I3	Q9lti3 tupaya herp
20	8	2.4	141	6	Q95J85	Q95j85 monodelphis
21	8	2.4	142	4	Q8WW60	Q8ww60 homo sapien
22	8	2.4	153	10	Q9XG81	Q9xg81 oryza sativ
23	8	2.4	179	2	Q93Q47	Q93q47 clostridium
24	8	2.4	190	4	Q8TBP5	Q8tbp5 homo sapien
25	8	2.4	197	11	Q64697	Q64697 mus musculu
26	8	2.4	200	11	Q9CRN2	Q9crn2 mus musculu
27	8	2.4	205	10	Q9LZ12	Q9lzl2 arabidopsi
28	8	2.4	206	4	Q14761	Q14761 homo sapien
29	8	2.4	221	11	Q9D8Y6	Q9d8y6 mus musculu
30	8	2.4	230	13	Q9PU48	Q9pu48 gallus gall
31	8	2.4	254	4	Q9H2F6	Q9h2f6 homo sapien
32	8	2.4	254	4	Q9BXD6	Q9bx66 homo sapien
33	8	2.4	283	11	Q60819	Q60819 mus musculu
34	8	2.4	267	4	Q13261	Q13261 homo sapien
35	8	2.4	273	4	Q96K63	Q96k63 homo sapien
36	8	2.4	273	4	Q8TC80	Q8tc80 homo sapien
37	8	2.4	290	17	Q82X93	Q82x93 pyrobaculum
38	8	2.4	301	4	Q96K94	Q96k94 homo sapien
39	8	2.4	301	4	Q8TDQ0	Q8tdq0 homo sapien
40	8	2.4	307	11	Q922Q8	Q922q8 mus musculu
41	8	2.4	315	11	Q35783	Q35783 rattus norv
42	8	2.4	316	11	P89000	P89000 praonys nat
43	8	2.4	376	8	Q94V43	Q94v43 tamlas stri
44	8	2.4	376	10	O24579	O24579 zea mays (m
45	8	2.4	377	4	Q8TAG4	Q8tag4 homo sapien

ALIGNMENTS

RESULT 1

Q96D15
ID Q96D15 PRELIMINARY; PRT; 328 AA.
AC Q96D15;
CT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 37.5 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013436; AAH13436.1; -
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; EF_target.
DR Pfam; PF00036; ehand; 5.
DR PROSITE; PS00018; EF_HAND; UNKNOWN 4.
DR PROSITE; PS00014; EF_TARGET; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 328 AA; 37493 MW; B64EDB28B961088D CRC64;

Query Match 100.0%; Score 328; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MMWRPSVLLLLLRHGAQKSPDAGPHQGRVHQAPLSDAPHDAGHGNFYDHEAFL 60
Db	1	MMWRPSVLLLLLRHGAQKSPDAGPHQGRVHQAPLSDAPHDAGHGNFYDHEAFL 60
Qy	61	GREVAKFEDLTPEESQARLGRIVDRMDRAGDGDGWVSLAEALRAWTAAHTQQRHRSVSA 120
Db	61	GREVAKFEDLTPEESQARLGRIVDRMDRAGDGDGWVSLAEALRAWTAAHTQQRHRSVSA 120
Qy	121	AWDTYDTRDGRVGEELRNATYGHYAPGEEFHVDVDAETKKMLARDRRFRVADQDGD 180

Tue May 20 14:43:22 2003

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DB 121 AWDYIDRGRVGEELRNATYGHVAPGEEHDEDAETKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAFLPEEPHMRDIVIAETLEDLDRKNGYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLPEEPHMRDIVIAETLEDLDRKNGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WYQTERQFRDLNKGDLGSGEVHVLPPAQDQPLVEANHLHESDTDKDGRLSKA 300
DB 241 WYQTERQFRDLNKGDLGSGEVHVLPPAQDQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNMNFVGSQATNYGDELTRHDEL 328
DB 301 EILGNMNFVGSQATNYGDELTRHDEL 328

RESULT 2
Q9HBZ8 PRELIMINARY; PRT; 328 AA.
AC Q9HBZ8;
DT 01-JUN-2001 (TRENBLrel. 16, Created)
DT 01-JUN-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Reticulocabin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=HYPOTHALAMUS;
RA Feng Y., Gu Y., Huang C., Xu S., Han Z., Fu G., Chen Z.;
RT "A novel gene expressed in human hypothalamus.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF183423; AAG09692.1; -
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000886; ER-target.
DR Pfam: PF00036; ehand; 4.
DR SMART: SM00054; EFN; 3.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 328 AA; 37424 MW; 9D23648795D3C670 CRC64;

Query Match 71.6%; Score 235; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 2e-232;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 DGWYSLAEALRAWIAHTQQRHRSVSAAWDTYDTRDGRVGEELRNATYGHVAPGEEPH 153
DB 94 DGWYSLAEALRAWIAHTQQRHRSVSAAWDTYDTRDGRVGEELRNATYGHVAPGEEPH 153
QY 154 DVEAETKKMLARDERRFRVADQDGSMTARELTAFLEHPEEPHMRDIVIAETLEDLD 213
DB 154 DVEAETKKMLARDERRFRVADQDGSMTARELTAFLEHPEEPHMRDIVIAETLEDLD 213
QY 214 RNKDGQYVQVEEYIADLYSAEPGEEPAWQTERQFRDLNKGDLGSGEVHVLPP 273
DB 214 RNKDGQYVQVEEYIADLYSAEPGEEPAWQTERQFRDLNKGDLGSGEVHVLPP 273
QY 274 AQDQPLVEANHLHESDTDKDGRLSKAELGNMNFVGSQATNYGDELTRHDEL 328
DB 274 AQDQPLVEANHLHESDTDKDGRLSKAELGNMNFVGSQATNYGDELTRHDEL 328

RESULT 3
Q9CTD4 PRELIMINARY; PRT; 259 AA.
AC Q9CTD4;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE 6030455P07Rik protein (Fragment).
GN 6030455P07RIK.

```

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli J., Gariboldi M.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Tovo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK003918; BAB23076.1; -
DR MGD: MGI:1915346; 6030455P07RIK.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000886; ER-target.
DR Pfam: PF00036; ehand; 4.
DR SMART: SM00054; EFN; 3.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 259 AA; 30163 MW; 7910A9F0476260A1 CRC64;

Query Match 17.4%; Score 57; DB 11; Length 259;
Best Local Similarity 100.0%; Pred. No. 6.9e-50;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 PGEFHVDVDEATYKKMLARDERRFRVADQDGSMTARELTAFLEHPEEPHMRDIV 204
DB 79 PGEFHVDVDEATYKKMLARDERRFRVADQDGSMTARELTAFLEHPEEPHMRDIV 135

RESULT 4
Q99K35 PRELIMINARY; PRT; 315 AA.
ID Q99K35;
AC Q99K35;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Similar to hypothetical protein LOC57333 (Fragment).
GN 6030455P07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005487; AAH05487.1; -
DR MGD: MGI:1915346; 6030455P07RIK.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000886; ER-target.
DR Pfam: PF00036; ehand; 4.
DR SMART: SM00054; EFN; 3.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.

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KW Hypothetical protein.

FT NON_TER 1
SQ SEQUENCE 315 AA; 36269 MW; CECE4DAE54D24E4 CRC64;

Query Match 17.4%; Score 57; DB 11; Length 315;
Best Local Similarity 100.0%; Pred. No. 8.2e-50;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 PGEFHVDVDAETKKMLARDERRFRVADQDGDGSMATREELTAFLHPPEFPHMRDIV 204
Db 135 PGEFHVDVDAETKKMLARDERRFRVADQDGDGSMATREELTAFLHPPEFPHMRDIV 191

RESULT 5

Q8R137
ID Q8R137 PRELIMINARY; PRT; 328 AA.
AC Q8R137;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to hypothetical protein LOC57333.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025602; AAH25602.1; -.
KW Hypothetical protein.
SQ SEQUENCE 328 AA; 37973 MW; 913F5C6F0F8B316 CRC64;

Query Match 17.4%; Score 57; DB 11; Length 328;
Best Local Similarity 100.0%; Pred. No. 8.5e-50;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 PGEFHVDVDAETKKMLARDERRFRVADQDGDGSMATREELTAFLHPPEFPHMRDIV 204
Db 148 PGEFHVDVDAETKKMLARDERRFRVADQDGDGSMATREELTAFLHPPEFPHMRDIV 204

RESULT 6

Q63399
ID Q63399 PRELIMINARY; PRT; 98 AA.
AC Q63399;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE (clone REM1) ORF (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-HOLZMAN; TISSUE-BRAIN;
RX MEDLINE=96235155; PubMed=8642059;
RA Asakura K., Pogulis R.J., Pease L.R., Rodriguez M.;
RT "A monoclonal autoantibody which promotes central nervous system remyelination is highly polyreactive to multiple known and novel antigens."
RT J. Neuroimmunol. 65:11-19(1996).
DR EMBL; L41683; AAB05841.1;
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; ehand; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 98
SQ SEQUENCE 98 AA; 11277 MW; F0A3D6D9EF624CE1 CRC64;

Query Match 7.6%; Score 25; DB 11; Length 98;
Best Local Similarity 100.0%; Pred. No. 2e-17;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 64 VAKFEDQLTPESQARLGRIIVDRMD 88
Db 4 VAKFEDQLTPESQARLGRIIVDRMD 28

RESULT 7

O93434
ID O93434 PRELIMINARY; PRT; 322 AA.
AC O93434;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Reticulocalbin.
GN RCN1.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99007268; PubMed=9789042;
RA Miles C., Elgar G., Coles E., Kleinjan D.J., Van Heyningen V.,
RA Hastie N.;
RT "Complete sequencing of the Fugu WAGR region from WT1 to PAX6:
RT Dramatic compaction and conservation of synteny with human chromosome
RT 11p13".
RL PROC. Natl. Acad. Sci. U.S.A. 95:13068-13072(1998).
DR EMBL; AL021531; CAA16492.1; -.
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; ehand; 5.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 322 AA; 38207 MW; 85F99C053AC34C5C CRC64;

Query Match 5.8%; Score 19; DB 13; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 NWNMFVGSQATNYGEDLTR 323
Db 299 NWNMFVGSQATNYGEDLTR 317

RESULT 8

Q9Y303
ID Q9Y303 PRELIMINARY; PRT; 217 AA.
AC Q9Y303;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE P24B protein precursor (Integral type I protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-PLACENTA;
RA Blum R., Nastainczyk W., Kohler B., Schulz I.;
RT "Cloning, localization and in vivo trafficking of p24B, a novel p24-
RT member."
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Carim L., Estivill X., Sumoy L., Escarceller M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]

RP	SEQUENCE FROM N.A.
RP	Auffray C., Ansoerge W., Ballabio A., Estivill X., Gibson K.,
RA	Lehrach H., Poustka A., Lundeberg J.;
RA	"The European IMAGE consortium for integrated Molecular analysis of
RT	"human gene transcripts.";
RT	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RL	[4]
RP	SEQUENCE FROM N.A.
RP	TISSUE-KIDNEY;
RA	Strausberg R.;
RA	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RL	[5]
RP	SEQUENCE FROM N.A.
RP	TISSUE-LUNG;
RA	Strausberg R.;
RA	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL	[6]
RP	SEQUENCE FROM N.A.
RP	TISSUE-SKIN;
RA	Strausberg R.;
RA	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RL	[7]
RP	SEQUENCE FROM N.A.
RP	TISSUE-LUNG;
RC	RC

RA	Strausberg K. (Feb. 2002)	to the EMBL/GenBank/DBJ databases.
DR	Submitted	-
DR	EMBL: AJ132270	CAB40416.1
DR	EMBL: AJ109672	CAB52017.1
DR	EMBL: BC000027	AAH00027.1
DR	EMBL: BC010853	AAH10853.1
DR	EMBL: BC017495	AAH17495.1
DR	EMBL: BC022332	AAH22332.1

[illegible]

RESULT	ID	Q8VAZ4	PRELIMINARY;	PRT;	269 AA.
Q8VAZ4	Q8VAZ4				
AC	Q8VAZ4;				
DT	01-MAR-2002	(TREMBlrel. 20, Created)			
DT	01-MAR-2002	(TREMBlrel. 20, Last sequence update)			
DT	01-JUN-2002	(TREMBlrel. 21, Last annotation update)			
DE	Wsv221 (WSSV276).				
OS	White spot syndrome virus (WSSV).				
OC	Viruses; unclassified viruses.				
OX	NCBI_TaxID=92652;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21548311; PubMed=11689662;				
RA	Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;				
RT	"Complete genome sequence of the shrimp white spot bacilliform virus.";				
RT	J. Virol. 75:11811-11820(2001).				

KN [2]
 RP SEQUENCE FROM N.A.
 RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

Db 42 FDQLTPEES 50
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RESULT 11

Q9M246
ID Q9M246 PRELIMINARY; PRT; 296 AA.
AC Q9M246
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Crocalbin-like protein (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=99192326; PubMed=10094503;
RA Hsue M.J., Yen C.H., Tzeng M.C.;
RT "Crocalbin: a new calcium-binding protein that is also a binding
RT protein for crotoxin, a neurotoxic phospholipase A2.";
RL FEBS Lett. 445:440-444(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Hsue M.J., Tzeng M.C.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF257660; AAF76142.1;
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; ehand; 6.
DR SMART: SM00054; EFH; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
FT NON_TER 1
FT 296
SQ SEQUENCE 296 AA; 34896 MW; 7C01BB38C6275914 CRC64;

Query Match 2.7%; Score 9; DB 6; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 FDQLTPEES 76
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RESULT 12

Q96RL3
ID Q96RL3 PRELIMINARY; PRT; 315 AA.
AC Q96RL3
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Calumenin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Peterson R.E. Jr., Watson D.K.;
RT "Novel splice variant of human calumenin.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF345637; AAK72908.1;
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; ehand; 6.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 315 AA; 37135 MW; E1BF415B25076676 CRC64;

Query Match 2.7%; Score 9; DB 4; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 FDQLTPEES 76
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Db 61 FDQLTPEES 69

RESULT 13

Q9ESQ6
ID Q9ESQ6 PRELIMINARY; PRT; 26 AA.
AC Q9ESQ6
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Prostacyclin synthase (Fragment).
GN PTGIS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129SVJ; TISSUE=SPLEEN;
RA Okawara S., Shimonishi M., Tanabe T., Yokoyama C.;
RT "Cloning and characterization of 5'-flanking region of mouse
RT prostacyclin synthase gene.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040750; BAB12574.1;
DR MGD; MGI:1097156; Ptgis.
KW Cyclin
FT NON_TER 26
FT 26
SQ SEQUENCE 26 AA; 2933 MW; 7C110848736AB9E0 CRC64;

Query Match 2.4%; Score 8; DB 11; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VLLLLLLL 14
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Db 12 VLLLLLLL 19

RESULT 14

Q9JHO7
ID Q9JHO7 PRELIMINARY; PRT; 58 AA.
AC Q9JHO7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Laminin alpha 3B chain precursor (Fragment).
GN LAMA3B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21818471; PubMed=11829758;
RA Garbe J.H.O., Gohring W., Mann K., Timpl R., Sasaki T.;
RT "Complete sequence, recombinant analysis and binding to Laminins and
RT sulfated ligands of the N-terminal domains of Laminin alpha 3B and
RT alpha 5 chains.";
RL Biochem. J. 362:213-221(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Friedrich W.V.K.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ293592; CAB99254.2;
KW SIGNAL
FT SIGNAL 1 31
FT CHAIN 32 >58 LAMININ ALPHA 3B CHAIN.
FT NON_TER 58
FT 58
SQ SEQUENCE 58 AA; 6464 MW; 96BB58C75E8C427F CRC64;

Tue May 20 14:43:22 2003

Query Match 2.4%; Score 8; DB 11; Length 58;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLLLLLL 15
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 Db 18 LLLLLLL 25

RESULT 15
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 AC Q9NLYO
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE Hypothetical 6.7 kDa protein (Fragment).
 GN LM26.312.
 OS Leishmania major.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL160493; CAB97930.1;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 62 AA; 6695 MW; BBC186B54327F894 CRC64;

Query Match 2.4%; Score 8; DB 5; Length 62;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLL 14
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 Db 52 VLLLLLL 59

Search completed: May 14, 2003, 10:49:40
 Job time : 36 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:47:58 ; Search time 14 Seconds
(without alignments)
689.337 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 328
Sequence: 1 MMWRPSVLLLLLLRHGAQG.....FVGSQATNYGDLFRHHDEL 328

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES										
Result No.	Score	Query %		Length	DB	ID	Description			
		Match								
1	328	100.0	328	2	US-08-828-242-1	Sequence 1, Appli				
2	328	100.0	328	2	US-08-910-927B-1	Sequence 1, Appli				
3	328	100.0	328	4	US-09-206-499-1	Sequence 1, Appli				
4	328	100.0	328	4	US-09-270-270-1	Sequence 1, Appli				
5	25	7.6	98	2	US-08-910-927B-6	Sequence 6, Appli				
6	25	7.6	98	4	US-09-270-270-6	Sequence 6, Appli				
7	18	5.5	325	2	US-08-828-242-4	Sequence 4, Appli				
8	18	5.5	325	4	US-09-206-499-4	Sequence 4, Appli				
9	18	5.5	331	2	US-08-828-242-3	Sequence 3, Appli				
10	18	5.5	331	2	US-08-910-927B-5	Sequence 5, Appli				
11	18	5.5	331	4	US-09-206-499-3	Sequence 3, Appli				
12	18	5.5	331	4	US-09-270-270-5	Sequence 3, Appli				
13	9	2.7	315	2	US-08-910-927B-3	Sequence 3, Appli				
14	9	2.7	315	4	US-09-270-270-3	Sequence 3, Appli				
15	8	2.4	21	3	US-08-848-580-6	Sequence 6, Appli				
16	8	2.4	21	3	US-08-848-580-7	Sequence 7, Appli				
17	8	2.4	21	5	PCT-US92-04537-2	Sequence 2, Appli				
18	8	2.4	21	5	PCT-US92-04537-3	Sequence 3, Appli				
19	8	2.4	45	1	US-08-056-200-107	Sequence 107, App				
20	8	2.4	45	2	US-08-800-644-107	Sequence 107, App				
21	8	2.4	54	1	US-08-464-339A-15	Sequence 15, Appl				
22	8	2.4	89	1	US-07-987-272A-10	Sequence 10, Appl				
23	8	2.4	90	4	US-09-370-838-200	Sequence 200, App				
24	8	2.4	206	1	US-08-197-793-2	Sequence 2, Appli				
25	8	2.4	206	2	US-08-636-176-2	Sequence 2, Appli				
26	8	2.4	206	5	PCT-US95-01618-2	Sequence 2, Appli				
27	8	2.4	234	1	US-08-300-903A-11	Sequence 11, Appli				

28 8 2.4 251 1 US-08-300-903A-7 Sequence 7, Appli
29 8 2.4 254 4 US-09-449-437A-4 Sequence 4, Appli
30 8 2.4 254 4 US-09-449-437A-6 Sequence 6, Appli
31 8 2.4 254 4 US-09-195-106-2 Sequence 2, Appli
32 8 2.4 263 1 US-08-300-903A-2 Sequence 2, Appli
33 8 2.4 267 1 US-08-300-903A-15 Sequence 15, Appli
34 8 2.4 279 1 US-08-300-903A-9 Sequence 9, Appli
35 8 2.4 301 3 US-08-829-525-24 Sequence 24, Appli
36 8 2.4 301 4 US-08-609-583A-24 Sequence 24, Appli
37 8 2.4 301 4 US-08-937-399-24 Sequence 24, Appli
38 8 2.4 301 4 US-09-310-367-24 Sequence 24, Appli
39 8 2.4 301 4 US-09-032-337-24 Sequence 24, Appli
40 8 2.4 351 1 US-08-458-847B-16 Sequence 16, Appli
41 8 2.4 361 1 US-08-415-751-36 Sequence 36, Appli
42 8 2.4 385 4 US-09-163-951-16 Sequence 16, Appli
43 8 2.4 447 1 US-07-937-609-29 Sequence 29, Appli
44 8 2.4 447 1 US-07-978-892A-6 Sequence 6, Appli
45 8 2.4 447 4 US-08-029-170-29 Sequence 29, Appli

ALIGNMENTS

RESULT 1
US-08-828-242-1
; Sequence 1, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filled Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CONUTUT01
; CLONE: 2509570
US-08-828-242-1

Query Match 100.0%; Score 328; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.4e-299;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MMWRP	SVLLLLLLRRGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFL	60
Db	1	MMWRP	SVLLLLLLRRGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFL	60
QY	61	GREVAKE	FQDLTPESQARLGRIVRMDRAGDGDGHWVSLAELRAWTAHTQQORHIDSVSA	120
Db	61	GREVAKE	FQDLTPESQARLGRIVRMDRAGDGDGHWVSLAELRAWTAHTQQORHIDSVSA	120
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Db	121	AWDTY	TDTRDGRVGEWELRNATYGHVAPGEEFHDVDEAETYKKMLARDERRFRVADQGD	180
QY	181	SMATRE	LTAFLHPEBFFPHMRDVIATETLEDLDRNKDGVQVVEEYIADLYSAPEEPEPA	240
Db	181	SMATRE	LTAFLHPEBFFPHMRDVIATETLEDLDRNKDGVQVVEEYIADLYSAPEEPEPA	240
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Db	241	WVQTER	QOQFDFDLNKGDLGDSGVGHVWVLPQAQDQPIVEANHLHESDTPDKDGLSKA	300
QY	301	EILGN	NNMNFVGSQATNYGEDLTRHHDEL	328
Db	301	EILGN	NNMNFVGSQATNYGEDLTRHHDEL	328

RESULT 2
US-08-910-927B-1
Sequence 1, Application US/08910927B
Patent No. 5976801
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 317A Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910, 927B
FILING DATE: Hereewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0358 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: RATRNOT02

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301 EILGNWNMFVGSQATNYGDLTRHHDEL 328
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301 EILGNWNMFVGSQATNYGDLTRHHDEL 328
Db

RESULT 3
US-09-206-499-1
: Sequence 1, Application US/09206499
: Patent No. 6194385
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Goll, Surya K.
: TITLE OF INVENTION: NOVEL CALCIUM-BINDING
: TITLE OF INVENTION: PROTEIN
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/206,499
: FILING DATE:
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/828,242
: FILING DATE: 03/31/1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0261 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 328 amino acids
: TYPE: amino acid
: STRANDEDNESS: single

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;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: CONUTUT01
;; CLONE: 2509570
US-09-206-499-1

Query Match 100.0%; Score 328; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.4e-299;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MMWRPSVLLLLLRHGAQCKSPDAGPHGQGRVHQAAAPLSDAPHDDAHGNGFYDHEAFL 60
Qy 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGVSLAELRAWIAHTQORHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGVSLAELRAWIAHTQORHIRDSVSA 120
Qy 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETTKMLARDERRFRVADODGD 180
Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETTKMLARDERRFRVADODGD 180
Qy 181 SMATREELTAFLHPPEFPHMRDVIATETLEDLRNKGYYQVVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPPEFPHMRDVIATETLEDLRNKGYYQVVEEYIADLYSAEPGEEPA 240
Qy 241 WYQTERQOFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WYQTERQOFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
Qy 301 EILGNWNVGVSQATNYGEDLTRHDEL 328
Db 301 EILGNWNVGVSQATNYGEDLTRHDEL 328

RESULT 4
US-09-270-270-1
; Sequence 1, Application US/09270270
; Patent No. 6235477
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,270
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,927
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166

;; TELEX:
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 328 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: RATRNOT02
;; CLONE: 922578
US-09-270-270-1

Query Match 100.0%; Score 328; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.4e-299;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MMWRPSVLLLLLRHGAQCKSPDAGPHGQGRVHQAAAPLSDAPHDDAHGNGFYDHEAFL 60
Db 1 MMWRPSVLLLLLRHGAQCKSPDAGPHGQGRVHQAAAPLSDAPHDDAHGNGFYDHEAFL 60
Qy 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGVSLAELRAWIAHTQORHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGVSLAELRAWIAHTQORHIRDSVSA 120
Qy 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETTKMLARDERRFRVADODGD 180
Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETTKMLARDERRFRVADODGD 180
Qy 181 SMATREELTAFLHPPEFPHMRDVIATETLEDLRNKGYYQVVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPPEFPHMRDVIATETLEDLRNKGYYQVVEEYIADLYSAEPGEEPA 240
Qy 241 WYQTERQOFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WYQTERQOFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
Qy 301 EILGNWNVGVSQATNYGEDLTRHDEL 328
Db 301 EILGNWNVGVSQATNYGEDLTRHDEL 328

RESULT 5
US-08-910-927B-6
; Sequence 6, Application US/08910927B
; Patent No. 5976801
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,927B
; FILING DATE: Hereafter
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

DB 302 RNNMFWOSQJNLCZ
RESULT 8
US-09-206-499-4
; Sequence 4, Application US/09206499
; patent No. 6194385


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; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/206,499
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,242
; FILING DATE: 03/31/1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 220582
; US-09-206-499-4

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Query Match 5.5%; Score 18; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 305 NNNMFVGSQATNYGDLT 322
DB 302 NNNMFVGSQATNYGDLT 319

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RESULT 9
US-08-828-242-3
; Sequence 3, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS

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; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filed Hereewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1262329
; US-08-828-242-3

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Query Match 5.5%; Score 18; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 305 NNNMFVGSQATNYGDLT 322
DB 308 NNNMFVGSQATNYGDLT 325

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RESULT 10
US-08-910-927B-5
; Sequence 5, Application US/08910927B
; Patent No. 5976801
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,927B
; FILING DATE: Hereewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166

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QV 305 NWNMFVGSQATNYGEDLT 322 QV


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; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910.927B
; FILING DATE: Hereewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADNOT03
; CLONE: 1601793
; US-09-910-927B-3

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Query Match 2.7%; Score 9; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 68 FQDLTPES 76
Db 61 FQDLTPES 69

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RESULT 15

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; US-08-848-580-6
; Sequence 6, Application US/08848580
; Patent No. 6013619
; GENERAL INFORMATION:
; APPLICANT: Cochran, Charles G
; APPLICANT: Revak, Susan D
; TITLE OF INVENTION: NOVEL PULMONARY SURFACTANTS AND
; TITLE OF INVENTION: THERAPEUTIC USES, INCLUDING PULMONARY LAVAGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10550 No. 6013619th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/848,580
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/488,123
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/419,824
; FILING DATE: 11-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,833
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/715,397
; FILING DATE: 14-JUN-1991

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Query Match 2.7%; Score 9; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 68 FQDLTPES 76
Db 61 FQDLTPES 69

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RESULT 14

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; US-09-270-270-3
; Sequence 3, Application US/09270270
; Patent No. 6235477
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0

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us-09-768-840-1.oli.ra1

Tue May 20 14:43:20 2003

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; PRIOR APPLICATION DATA: US 07/293,201
; APPLICATION NUMBER:
; FILING DATE: 04-JAN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/141,200
; FILING DATE: 06-JAN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 147.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-784-2937
; TELEFAX: 619-784-9399
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-848-580-6
;
; Query Match 2.4%; Score 8; DB 3; Length 21;
; Best Local Similarity 100.0%; Pred. No. 0.98;
; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 8 LLLLLLL 15
; Db 3 LLLLLLL 10
;
; Search completed: May 14, 2003, 10:50:27
; Job time : 15 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:48:43 ; Search time 23 Seconds
(without alignments)
1312.367 Million cell updates/sec

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Perfect score: 328
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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 349150 seqs, 92025710 residues

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Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Database : PublishedApplications_AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	328	100.0	328	9	US-09-902-853-221
3	328	100.0	328	9	US-09-907-824-221
4	328	100.0	328	9	US-09-907-841-221
5	328	100.0	328	9	US-09-904-011-221
6	328	100.0	328	9	US-10-028-072-364
7	328	100.0	328	9	US-09-906-742-221
8	328	100.0	328	9	US-10-121-045-364
9	328	100.0	328	9	US-10-123-904-364
10	328	100.0	328	9	US-10-140-470-364
11	328	100.0	328	9	US-09-906-838-221
12	328	100.0	328	9	US-09-907-613-221
13	328	100.0	328	9	US-09-907-942-221
14	328	100.0	328	9	US-10-175-746-364
15	328	100.0	328	9	US-10-176-918-364
16	328	100.0	328	9	US-10-176-921-364
17	328	100.0	328	9	US-10-137-865-364
18	328	100.0	328	9	US-10-140-474-364
19	328	100.0	328	9	US-09-904-820-221

20	328	100.0	328	9	US-09-904-859-221	Sequence 221, App
21	328	100.0	328	9	US-09-909-204-221	Sequence 221, App
22	328	100.0	328	9	US-10-142-431-364	Sequence 364, App
23	328	100.0	328	9	US-10-143-114-364	Sequence 221, App
24	328	100.0	328	9	US-09-904-786-221	Sequence 221, App
25	328	100.0	328	9	US-09-906-646-221	Sequence 221, App
26	328	100.0	328	9	US-09-906-700-221	Sequence 221, App
27	328	100.0	328	9	US-10-140-002-364	Sequence 364, App
28	328	100.0	328	9	US-09-902-903-221	Sequence 221, App
29	328	100.0	328	9	US-09-903-749A-221	Sequence 221, App
30	328	100.0	328	9	US-09-903-786-221	Sequence 221, App
31	328	100.0	328	9	US-10-142-419-364	Sequence 364, App
32	328	100.0	328	9	US-09-902-736-221	Sequence 221, App
33	328	100.0	328	9	US-09-904-119-221	Sequence 221, App
34	328	100.0	328	9	US-09-904-956-221	Sequence 221, App
35	328	100.0	328	9	US-09-907-794-221	Sequence 221, App
36	328	100.0	328	9	US-10-123-262-364	Sequence 364, App
37	328	100.0	328	9	US-10-142-423-364	Sequence 364, App
38	328	100.0	328	9	US-09-902-692-221	Sequence 221, App
39	328	100.0	328	9	US-09-903-520-221	Sequence 221, App
40	328	100.0	328	9	US-09-903-943-221	Sequence 221, App
41	328	100.0	328	9	US-09-904-463-221	Sequence 221, App
42	328	100.0	328	9	US-09-905-056-221	Sequence 221, App
43	328	100.0	328	9	US-09-907-925-221	Sequence 221, App
44	328	100.0	328	9	US-10-121-050-364	Sequence 364, App
45	328	100.0	328	9	US-10-141-755-364	Sequence 364, App

ALIGNMENTS

RESULT 1

US-09-905-291A-221
; Sequence 221, Application US/0905291A
; Patent No. US20020160374A1

GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222

APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
US-09-905-291A-221

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
DB 1 MMWRPSVLLLLLRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
QY 61 GREVAKEFQDLTPESQARLGRIVDRMDRAGDGDGVSVLAELRAWIAHTQQRHIRDSVSA 120
DB 61 GREVAKEFQDLTPESQARLGRIVDRMDRAGDGDGVSVLAELRAWIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRVGVWELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFVADODGD 180
DB 121 AWDYTDTRDGRVGVWELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFVADODGD 180
QY 181 SMATRELTAFHPPEFPHMRDIVIAETLEDLRNKGDVYQVEEYIADLYSAEPGEEPA 240
DB 181 SMATRELTAFHPPEFPHMRDIVIAETLEDLRNKGDVYQVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQQFRDLNKGDLGDSYGVHWYLPAPQDQPLVEANHLHESDTDKGRLSKA 300
DB 241 WVQTERQQFRDLNKGDLGDSYGVHWYLPAPQDQPLVEANHLHESDTDKGRLSKA 300
QY 301 EILGNWNNFVGSQATNYGDLTRHDEL 328
DB 301 EILGNWNNFVGSQATNYGDLTRHDEL 328

RESULT 2
US-09-902-853-221
Sequence 221, Application US/09902853
Publication No. US20030192659A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
DB 1 MMWRPSVLLLLLRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60

Qy 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
Qy 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADATYKKMLARDERRFRVADQDGD 180
Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADATYKKMLARDERRFRVADQDGD 180
Qy 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
Qy 241 WQTERQOQFRDRLNKGHLDSGVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WQTERQOQFRDRLNKGHLDSGVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Qy 301 EILGNWNNFVGSQATNYGDELTRHDEL 328
Db 301 EILGNWNNFVGSQATNYGDELTRHDEL 328

RESULT 3

US-09-907-824-221

; Sequence 221, Application US/09907824

; Publication No. US20020197671A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/907,824

; CURRENT FILING DATE: 2001-07-17

; PRIOR FILING DATE: 2000-09-18

; PRIOR FILING DATE: 2000-09-18

; PRIOR FILING DATE: 2000-09-18

; PRIOR FILING DATE: 2000-02-22

; PRIOR FILING DATE: 1999-07-07

; PRIOR FILING DATE: 1999-07-26

; PRIOR FILING DATE: 1999-07-26

; PRIOR FILING DATE: 1999-07-28

; PRIOR FILING DATE: 1999-07-28

; PRIOR FILING DATE: 1999-09-08

; PRIOR FILING DATE: 1999-09-13

; PRIOR FILING DATE: 1999-09-13

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-221

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMWRPSVLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFL 60
Db 1 MMWRPSVLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFL 60
Qy 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
Qy 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADATYKKMLARDERRFRVADQDGD 180
Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADATYKKMLARDERRFRVADQDGD 180
Qy 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
Qy 241 WQTERQOQFRDRLNKGHLDSGVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WQTERQOQFRDRLNKGHLDSGVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Qy 301 EILGNWNNFVGSQATNYGDELTRHDEL 328
Db 301 EILGNWNNFVGSQATNYGDELTRHDEL 328

RESULT 4

US-09-907-841-221

; Sequence 221, Application US/09907841

; Publication No. US20020198366A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth, J.
 APPLICANT: Kijavin, Ivar J.
 APPLICANT: Mather, Jennie P.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William, I.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth, J.
 APPLICANT: Kijavin, Ivar J.
 APPLICANT: Mather, Jennie P.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William, I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: 10466-14
 CURRENT APPLICATION NUMBER: US/09/907,841
 PRIOR FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: US 60/143,048
 PRIOR FILING DATE: 1999-07-07
 PRIOR APPLICATION NUMBER: PCT/US99/20594
 PRIOR FILING DATE: 1999-09-08
 PRIOR APPLICATION NUMBER: PCT/US99/20944
 PRIOR FILING DATE: 1999-09-13
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/21547
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/23089
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: PCT/US99/28214
 PRIOR FILING DATE: 1999-11-29
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: 1999-11-30
 PRIOR APPLICATION NUMBER: PCT/US99/28564
 PRIOR FILING DATE: 1999-12-02
 PRIOR APPLICATION NUMBER: PCT/US99/28565
 PRIOR FILING DATE: 1999-12-02
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: 1999-12-16
 PRIOR APPLICATION NUMBER: PCT/US99/30911
 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: PCT/US99/30999
 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: PCT/US00/00219
 PRIOR FILING DATE: 2000-01-05


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; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-221

Query Match      100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.le-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLRHGAQCKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAPL 60
   |||||
Db 1 MMWRPSVLLLLLRHGAQCKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAPL 60
   |||||
QY 61 GREVAKFQDLTPESQARLGRIVDRMDRAGDGDGHSVLAELRAMTAHTQQRHIRDSVSA 120
   |||||
Db 61 GREVAKFQDLTPESQARLGRIVDRMDRAGDGDGHSVLAELRAMTAHTQQRHIRDSVSA 120
   |||||
QY 121 AWDYTDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
   |||||
Db 121 AWDYTDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
   |||||
QY 181 SMATREELTAFLHPEEFPHMRDIVTAETLEDLDRNKDGVVQVEEYIADLYSAEPGEERPA 240
   |||||
Db 181 SMATREELTAFLHPEEFPHMRDIVTAETLEDLDRNKDGVVQVEEYIADLYSAEPGEERPA 240
   |||||
QY 241 WYOTERQOQFRDLNKGHLDSGVGHVLPAPQDQPLVEANHLHESDTRDKGRLSKA 300
   |||||
Db 241 WYOTERQOQFRDLNKGHLDSGVGHVLPAPQDQPLVEANHLHESDTRDKGRLSKA 300
   |||||
QY 301 EILGNWNMFVGSQATNYGEDLTRHHDEL 328
   |||||
Db 301 EILGNWNMFVGSQATNYGEDLTRHHDEL 328
   |||||

RESULT 6
US-10-028-072-364
; Sequence 364, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1998-02-04

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
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; PRIOR FILING DATE: 1997-09-19
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; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/064809
; PRIOR FILING DATE: 1997-11-07
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; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069212
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069278
; PRIOR FILING DATE: 1997-12-11
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; PRIOR FILING DATE: 1997-12-11
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; PRIOR FILING DATE: 1997-12-16
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; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 60/073612
; PRIOR FILING DATE: 1998-02-04
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Tue May 20 14:43:21 2003

;; PRIOR APPLICATION NUMBER: 60/074086
;; PRIOR FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: 60/074092
;; PRIOR FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
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;; PRIOR APPLICATION NUMBER: 60/085149
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;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
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;; PRIOR FILING DATE: 1998-06-24
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;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;;
Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.le-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMWRPSVLLLLLLRHGAQKQSPDAGPHCGRHOAAPLSDAPHDDAHGNGFYDHEAFL 60
Db 1 MMWRPSVLLLLLLRHGAQKQSPDAGPHCGRHOAAPLSDAPHDDAHGNGFYDHEAFL 60
QY 61 GREVAKFEEDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHRSVSA 120
Db 61 GREVAKFEEDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHRSVSA 120
QY 121 AWDTYTDTRDGRVGVWEELRNATYGHYAPGEEFHVDVDAETYYKKMLARDERRFRVADQGD 180
Db 121 AWDTYTDTRDGRVGVWEELRNATYGHYAPGEEFHVDVDAETYYKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQQFRDRLNKDGLDGVSEVGHVWLPAPQDQDPLVEANHLHESDTDKDGRLSKA 300
Db 241 WVQTERQQFRDRLNKDGLDGVSEVGHVWLPAPQDQDPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNMNFVGSQATNYCEDLTRHDEL 328
Db 301 EILGNMNFVGSQATNYCEDLTRHDEL 328
RESULT 7
US-09-768-840-1.oli.rapb
US-09-906-742-221
Sequence 221, Application US/09906742
Publication No. US20030023054A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/906,742
 ; CURRENT FILING DATE: 2001-07-16
 ; PRIOR APPLICATION NUMBER: 09/665,350
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 221
 ; LENGTH: 328
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-906-742-221

Query Match 100.0%; Score 328; DB 9; Length 328;
 Best Local Similarity 100.0%; Pred. No. 1.1e-274;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMWRPSVLLLLLLLRHGAQCKPSDAGPHCGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
 DB 1 MMWRPSVLLLLLLLRHGAQCKPSDAGPHCGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
 QY 61 GREVAKFEDQLTPESQARLGRIVDRMDRAGDGGVSWLAELRAWIAHTQQRHSDVSA 120
 DB 61 GREVAKFEDQLTPESQARLGRIVDRMDRAGDGGVSWLAELRAWIAHTQQRHSDVSA 120
 QY 121 AWDTYDTRDRGRVGEELRNATYGHVAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
 DB 121 AWDTYDTRDRGRVGEELRNATYGHVAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
 QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGDSVGHVWLPAPQDQPLVEANHLHSDTDKDGRLSKA 300
 DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGDSVGHVWLPAPQDQPLVEANHLHSDTDKDGRLSKA 300
 QY 301 EILGNMNFVGSQATNYGDELTRHDEL 328
 DB 301 EILGNMNFVGSQATNYGDELTRHDEL 328

QY 241 WYOTERQOFRDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSDTDKDGRLSKA 300
 DB 241 WYOTERQOFRDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSDTDKDGRLSKA 300
 QY 301 EILGNMNFVGSQATNYGDELTRHDEL 328
 DB 301 EILGNMNFVGSQATNYGDELTRHDEL 328

RESULT 8

US-10-121-049-364
 ; Sequence 364, Application US/10121049
 ; Publication No. US2003002239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330RIC17
 ; CURRENT APPLICATION NUMBER: US/10/121,049
 ; CURRENT FILING DATE: 2002-04-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 364
 ; LENGTH: 328
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-121-049-364

Query Match 100.0%; Score 328; DB 9; Length 328;
 Best Local Similarity 100.0%; Pred. No. 1.1e-274;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMWRPSVLLLLLLLRHGAQCKPSDAGPHCGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
 DB 1 MMWRPSVLLLLLLLRHGAQCKPSDAGPHCGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
 QY 61 GREVAKFEDQLTPESQARLGRIVDRMDRAGDGGVSWLAELRAWIAHTQQRHSDVSA 120
 DB 61 GREVAKFEDQLTPESQARLGRIVDRMDRAGDGGVSWLAELRAWIAHTQQRHSDVSA 120
 QY 121 AWDTYDTRDRGRVGEELRNATYGHVAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
 DB 121 AWDTYDTRDRGRVGEELRNATYGHVAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
 QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGDSVGHVWLPAPQDQPLVEANHLHSDTDKDGRLSKA 300
 DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGDSVGHVWLPAPQDQPLVEANHLHSDTDKDGRLSKA 300
 QY 241 WYOTERQOFRDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSDTDKDGRLSKA 300
 DB 241 WYOTERQOFRDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSDTDKDGRLSKA 300
 QY 301 EILGNMNFVGSQATNYGDELTRHDEL 328
 DB 301 EILGNMNFVGSQATNYGDELTRHDEL 328

Tue May 20 14:43:21 2003

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; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 364
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-140-470-364

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-274; Indels 0; Gaps 0;
Matches 328; Conservative 0; Mismatches 0;

QY 1 MMWRPSVLLLLLLLHGAQKSPDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAFL 60
Db 1 MMWRPSVLLLLLLLHGAQKSPDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWTIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWTIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRVGEELRNATYGHYAPGEEFHDVEAETYYKKMLARDERRFRVADODGD 180
Db 121 AWDYTDTRDGRVGEELRNATYGHYAPGEEFHDVEAETYYKKMLARDERRFRVADODGD 180
QY 181 SMATREELTAFLHPPEFPHMRDIVIAETLEDLDRNKDGYQVVEEYIADLYSAEPGEPEA 240
Db 181 SMATREELTAFLHPPEFPHMRDIVIAETLEDLDRNKDGYQVVEEYIADLYSAEPGEPEA 240
QY 241 WYOTERQQRFRDLNKGDLGSEVGHWWLPPAQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WYOTERQQRFRDLNKGDLGSEVGHWWLPPAQDQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNMNFVGSQATNYGDLTRHDEL 328
Db 301 EILGNMNFVGSQATNYGDLTRHDEL 328

RESULT 11
US-09-906-838-221
; Sequence 221, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 364
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-123-904-364

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-274; Indels 0; Gaps 0;
Matches 328; Conservative 0; Mismatches 0;

QY 1 MMWRPSVLLLLLLLHGAQKSPDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAFL 60
Db 1 MMWRPSVLLLLLLLHGAQKSPDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWTIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWTIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRVGEELRNATYGHYAPGEEFHDVEAETYYKKMLARDERRFRVADODGD 180
Db 121 AWDYTDTRDGRVGEELRNATYGHYAPGEEFHDVEAETYYKKMLARDERRFRVADODGD 180
QY 181 SMATREELTAFLHPPEFPHMRDIVIAETLEDLDRNKDGYQVVEEYIADLYSAEPGEPEA 240
Db 181 SMATREELTAFLHPPEFPHMRDIVIAETLEDLDRNKDGYQVVEEYIADLYSAEPGEPEA 240
QY 241 WYOTERQQRFRDLNKGDLGSEVGHWWLPPAQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WYOTERQQRFRDLNKGDLGSEVGHWWLPPAQDQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNMNFVGSQATNYGDLTRHDEL 328
Db 301 EILGNMNFVGSQATNYGDLTRHDEL 328

RESULT 10
US-10-140-470-364
; Sequence 364, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 364
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-123-904-364

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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-838-221

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1,1e-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMRPVSLLLLLLRGAQCKPSDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAPL 60
Db 1 MMRPVSLLLLLLRGAQCKPSDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAPL 60
QY 61 GREVAKFEQDLTPESQARLGRIVDRMDRAGDGDGWSLAELRAWTAHQRRHDSVSA 120
Db 61 GREVAKFEQDLTPESQARLGRIVDRMDRAGDGDGWSLAELRAWTAHQRRHDSVSA 120

QY 121 AWDYTDTRDGRVGEELRNATYGHYAPGEEFHVDVDAETKKMLARDERRFRVADQGD 180
Db 121 AWDYTDTRDGRVGEELRNATYGHYAPGEEFHVDVDAETKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEPEA 240
Db 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEPEA 240
QY 241 WVQTERQQFRDLNKNKGHDGSEVGHVWLPAPADQDPLVEANHLHSHESDTRDKDRLSKA 300
Db 241 WVQTERQQFRDLNKNKGHDGSEVGHVWLPAPADQDPLVEANHLHSHESDTRDKDRLSKA 300
QY 301 EILGNWNNFVGSQATNYGDLTRHDEL 328
Db 301 EILGNWNNFVGSQATNYGDLTRHDEL 328
RESULT 12
US-09-907-613-221
Sequence 221, Application US/09907613
Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,613
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313


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; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-907-613-221

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.le-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLHKGAGKPSDAGPGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
Db 1 MMWRPSVLLLLLHKGAGKPSDAGPGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
QY 61 GREVAKEFDQLTPESQARLGRIVDNRMDAGDGDGWVSLAELRAWTAAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPESQARLGRIVDNRMDAGDGDGWVSLAELRAWTAAHTQQRHIRDSVSA 120
QY 121 AMDTDTDRDGRVGEELRNATYGHYAPGEEFHVDDEATYKKMLARDERRFRVADQDGD 180
Db 121 AMDTDTDRDGRVGEELRNATYGHYAPGEEFHVDDEATYKKMLARDERRFRVADQDGD 180
QY 181 SMATREELTAFLHPEEFPHMRDVIETAETLEDLRNKGQYVQVVEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEFPHMRDVIETAETLEDLRNKGQYVQVVEYIADLYSAEPGEEPA 240
QY 241 WVQTERQQFRDRLNKGCHLDGSEVGHWVLPAPADQPLVEANHLHESDTRDKDGRLSKA 300
Db 241 WVQTERQQFRDRLNKGCHLDGSEVGHWVLPAPADQPLVEANHLHESDTRDKDGRLSKA 300
QY 301 EILGNWNMFVGSQATNYGEDLTRHDEL 328
Db 301 EILGNWNMFVGSQATNYGEDLTRHDEL 328

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US-09-907-942-221
 Commerce 221 Application US/09907942

US-09-907-942-221
: Sequence 221, Application US/09907942

Publication No. US20030027146A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: ASHKENAZI, AVI
APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoli
Fellneroff, Ell

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspe

; APPLICANT: Gerritsen, Mar

APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Chri

APPLICANT: Gurney, Austin

APPLICANT: Hillan, Kenneth

APPLICANT: KIJAVIN, IVAN
APPLICANT: Mather, Jennie

APPLICANT: Pan, James

10

Db 241 WYQTEROQFRDRLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Qy 301 EILGNMNFVGSQATNYGDELTRHDEL 328
Db 301 EILGNMNFVGSQATNYGDELTRHDEL 328

RESULT 14

US-10-175-746-364
; Sequence 364, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC353
; CURRENT APPLICATION NUMBER: US/10/175,746
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 364
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-364

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.le-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMWRPSVLLLLLLRHGAQKPSDPAGPHGQGRVHQAPLSDAPHDDAHGNFYDHEAFL 60
Db 1 MMWRPSVLLLLLLRHGAQKPSDPAGPHGQGRVHQAPLSDAPHDDAHGNFYDHEAFL 60
Qy 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
Qy 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
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RESULT 15

US-10-176-918-364
; Sequence 364, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 364
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-364

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.le-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: May 14, 2003, 10:50:56
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 22:09:52 ; Search time 3346 Seconds
(without alignments)
2852.875 Million cell updates/sec

Title: US-09-768-840-1

Perfect score: 328

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

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Total number of hits satisfying chosen parameters: 4106487

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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16: em_fun:*
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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	328	100.0	1055	6	AR035969	Sequence
2	328	100.0	1055	6	AR135029	Sequence
3	328	100.0	1463	6	AR083085	Sequence
4	328	100.0	1463	6	AR152960	Sequence
5	328	100.0	1470	9	BC0113436	Homo sapi
6	328	100.0	1503	6	AX464230	Sequence
7	300	91.5	1507	6	AX354366	Sequence
8	300	91.5	1507	6	AX354369	Sequence
9	235	71.6	1454	9	AF183423	Sequence
10	81	24.7	179394	9	AC010619	Homo sapi
11	65	19.8	658	6	AX354365	Sequence
12	57	17.4	1414	10	BC005487	Sequence
13	57	17.4	1421	10	BC025602	Sequence
14	57	17.4	110000	2	AC073763_0	Sequence
15	57	17.4	161995	2	AC099450	Rattus no
16	57	17.4	186243	2	AC073740	Mus muscu
17	57	17.4	191713	2	AC126256	Mus muscu
18	25	7.6	294	10	RATORF	L41683 Rattus norv
19	20	6.1	110000	2	AC073763_2	Continuation (3 of
20	19	5.8	45565	5	FR151J19	AL021531 Fugu rubr
21	18	5.5	408	6	AX351308	Sequence
22	18	5.5	411	6	AX341934	Sequence
23	18	5.5	501	6	AX331573	Sequence
24	18	5.5	1454	9	BC010120	Homo sapi
25	18	5.5	1998	10	MUSRCAL	D13003 Mus musculu
26	18	5.5	2104	6	AX330466	Sequence
27	18	5.5	2104	9	HUMRCN	D42073 Human mRNA
28	18	5.5	2416	9	AK094360	Sequence
29	18	5.5	2557	10	MUSRET15	AK094360 Homo sapi
30	18	5.5	44882	2	AC020850_4	D43956 Mouse gene
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43	13	4.0	250213	2	AC114695	AC129665 Rattus no
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ALIGNMENTS

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QY	261	LeuAspGlySerGluValGlyHisTyrValLeuProProAlaGlnAspGlnProLeuVal	280
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QY	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
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DEFINITION	Homo sapiens, hypothetical protein LOC57333, clone MGC:16899		
ACCESSION	BC013436		
VERSION	BC013436.1	GI:15488584	
KEYWORDS	MGC.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 1470)		
JOURNAL	Strausberg,R.		
	Direct Submission		
	Submitted (04-SEP-2001) National Institutes of Health, Mammalian		
	Gene Collection (MGC), Cancer Genomics Office, National Cancer		
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
	USA		
REMARK	NIH-MGC project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: DCTD/DP/Gapdar		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	cDNA Sequencing by: Sequencing Group at the Stanford Human Genome		
	Center, Stanford University School of Medicine, Stanford, CA 94305		
	Web site: http://www-shgc.stanford.edu		
	Contact: (Dickson, Mark) mcd@paxil.stanford.edu		
	Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,		
	R. M.		
	Clone distribution: MGC clone distribution information can be found		
	through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov		
	Series: IRAC Plate: 14 Row: d Column: 12		
	This clone was selected for full length sequencing because it		
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	location/qualifiers		

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DB:	9			
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US-09-768-840-1 (1-328) x BC013436 (1-1470)

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ACCESSION			
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AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
BASE COUNT			
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Pred. No.:			
Score:			
Percent Similarity:			
Best Local Similarity:			
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DB:			
US-09-768-840-1 (1-328) x AX464230 (1-1503)			

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US-09-768-840-1 (1-328) x AX464230 (1-1503)

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Qy	21	Lys	Pro	Ser	Pro	Asp	Ala	Gly	Pro	His	Gly	Gln	Gly	Arg	Val	His	Gln	Ala	Ala	Pro	Leu	40
Db	95	AGC	CAT	CCC	CAG	ACG	AGG	CCC	TCA	TGG	CGC	AGG	GAG	GGT	GC	ACC	AGC	GGC	GGC	CCC	CGT	154
Qy	41	Ser	Asp	Ala	Pro	His	Asp	Asp	Ala	His	Gly	Asn	Phe	Gln	Tyr	Asp	His	Gly	Ala	Phe	Leu	60
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Qy	61	Gly	Arg	Glu	Val	Ala	Lys	Gly	Phe	Asp	Asn	Leu	Thr	Pro	Glu	Glu	Ser	Gln	Ala	Arg	Leu	80
Db	215	GGC	CGG	AAAT	TGG	CAA	GAA	TTC	AC	CAACT	TAC	CCC	AG	AGG	AAAC	CGC	CGC	CTG	CTG	CTG	CTG	274

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	QY	101	GlulLeuArgAlaThrIleAlaHisThrGlnInArgHisIleAraGspSerValSerAla	120
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	QY	141	AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr	160
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	QY	161	TyrLysLysMetLeuAlaAraGspGluAraArgPheArgValAlaAraGspGlyLysP	180
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	QY	181	SerMetalThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
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	QY	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla	240
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	QY	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
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	VERSION	AX354366.1 GI:18619208		
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	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	REFERENCE	1		
	AUTHORS	Kennedy,G.C., Kang,S., Reinhard,C. and Jefferson,A.B.		
	TITLE	Polynucleotides related to colon cancer		
	JOURNAL	Patent: WO 0196523-A 12 20-DEC-2001;		
		CHIRON CORPORATION (US)		
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ACCESSION AX354365
VERSION AX354365.1 GI:18619207
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Kennedy,G.C., Kang,S., Reinhard,C. and Jefferson,A.B.
TITLE Polynucleotides related to colon cancer
JOURNAL Patent: WO 0196523-A 11 20-DEC-2001;
CHIRON CORPORATION (US)
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QY 284 HisLeuLeuHisGluSerAspThrAspGlyArgLeuSerLysAlaGluLeuLeu 303
Db 96 CACCTGCTGCAGAGCGACGACGAGCGGCGCTGAGCAACCGGAATCTCTG 155
QY 304 GlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAspLeuThrArg 323
Db 156 GGTAAATGGACATGTTTGGGCACTGAGCCACCACTATGTTGAGGACCTGACCCGG 215
QY 324 HisHisAspGluLeu 328
Db 216 CACCACGATGAGCTG 230
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BC005487
LOCUS
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ACCESSION BC005487
VERSION BC005487.1 GI:13529538
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1414)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer

```

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Lohar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Center, Stanford Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdepaxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 7 Row: h Column: 5
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES
 source Location/Qualifiers
 1..1414
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /map="CS7BL/6J"
 /clone="IMAGE:3486146"
 /tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months old, gross tissue."
 /clone_lib="NCI_CGAP_Mam5"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"
 <1..948
 /codon_start=1
 /product="Similar to hypothetical protein LOC57333"
 /protein_id="AAH05487.1"
 /db_xref="GI:13529539"
 /translation="LRHWALGKPSDPAGPHGQDRVHCTPLSEAPHDDAHGNFOYDHE
 AFLGRDVAKEFDKLSPEESQARLGRIVDRMLAGSDGWSLAELRAWIAHQQRHTR
 DVSAAWHTYDTRDRGQWELRNATYGHPEEFHDEDAETYYKKMLARERRR
 VADQDQSMATREELTALHPEEFPHMRDIIVAETLEDKNDGYVQVEEYADLYS
 EBPGRPPAWQTERQQFREFRDLNKDQSDGSEVGYWVLPSPDQDPLVEANILHES
 DTDGRLSKAEILSNWNWNVFGSATNNGEDLRRHDEL"
 BASE COUNT 422 a 384 c 392 g 216 t
 ORIGIN

Alignment Scores:
 Pred. No.: 6,24e-51 Length: 1414
 Score: 57.00 Matches: 57
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 17.38% Indels: 0
 DB: 10 Gaps: 0
 US-09-768-840-1 (1-328) x BC005487 (1-1414)
 QY 148 ProGlyGluGluPheHisAspValGluAspAlaGluThrTyrLysLysMetLeuAlaArg 167
 Db 403 CCCGAGAGGAGTTTCATGATGTGGAGATGCCGAGACCTACAGAAGATGCTGCTCGG 462
 QY 168 AspGluArgArgPheArgValAlaAspGlnAspGlyAspSerMetAlaThrArgGluGlu 187
 Db 463 GATGAGCGCGATTCCGGGTAGCCGACCAAGATGGGACTCCATGCTACTCGGGAAGAG 522
 QY 188 LeuThrAlaPheLeuHisProGluGluPheProHisMetArgAspIleVal 204
 Db 523 CTGACGCGCTTCTGCATCCCGAGGAGTTCCTCTACATCGGAGCATCGT 573
 RESULT 13
 BC025602
 LOCUS
 DEFINITION BC025602 Mus musculus, similar to hypothetical protein LOC57333, clone
 MGC:36253 IMAGE:5250505, mRNA, complete cds.

BC025602 1421 bp mRNA linear ROD 07-AUG-2002
 Mus musculus, similar to hypothetical protein LOC57333, clone
 MGC:36253 IMAGE:5250505, mRNA, complete cds.

us-09-768-840-1.0lip2n.rge

Tue May 20 14:43:22 2003

BC025602
 VERSION BC025602.1 GI:19343897
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE Strausberg, R.
 AUTHORS Direct Submission
 TITLE Submitted (06-WAR-2002) National Institutes of Health, Mammalian
 JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 REMARK Contact: MGC help desk
 COMMENT Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Lohar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 56 Row: 5 Column: 12
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis, GenomeScan gene prediction, similarity but not identity
 to protein.
 FEATURES Location/Qualifiers
 1. .1421
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 /db_xref="taxon:10090"
 /map="C57BL/6J"
 /clone="MGC:36253 IMAGE:5250505"
 /tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
 old, gross tissue."
 /clone_lib="NCI_CGAP_Mam5"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"
 76..1062
 /codon_start=1
 /product="Similar to hypothetical protein LOC57333"
 /protein_id="AAH25602.1"
 /db_xref="GI:19343898"
 /translation="MMWRSFLLILLIRHWAQKSPDAGPHGQVRHGTPLSEAP
 HDAGNFGYHEAFGLDVAKEFKLSPESQALRGIVDRMDLADSGDGNVSLAE
 RAWIAHQHRIHDSVSAWHTYDTDRGVGWEELRNATYHYEPGEFHDVEDAEI
 YKMLARDERFRVADQGDMSAPFEELTAFLPPEFPHMRDIVVAETLEDLKNKDG
 YVQVEYIADLYSEEPGEFPAWGTQEQREFEDLNKQGLDGSVGYWVLPSPQD
 QPLVEANILLHSDTKDGRKSAELLNNWNVGSQATNYGDLTRHDEL"
 BASE COUNT 335 a 414 c 427 g 245 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 6,27e-51 Length: 1421
 Score: 57.00 Matches: 57
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 17.38% Indels: 0
 DB: 10 Gaps: 0

US-09-768-840-1 (1-328) x BC025602 (1-1421)
 QY 148 ProGlyGluGluPheHisAspValGluaspAlaGluThrTyrLysMetLeuAlaarg 167
 Db 517 CCGGAGAGAGAGTTTCATGATGCGGATGCCGAGACCTACAGAGATGCTGCTCGG 576
 QY 168 AspGluArgArgPheArgValAlaAspGlnAspGlyAspSerMetAlaThrArgGluclu 187
 Db 577 GATGAGCGCGATTCGGGTAGCCGACCAAGATGGCGACTCCATCGCTACTCGGAAGAG 636
 QY 188 LeuThrAlaPheLeuHisProGluGluPheProHisMetArgAspIleVal 204
 Db 637 CTGACGCGCTTCTGATCCGAGGAGATTCCCTCATCATGCGGACATCGTG 687
 RESULT 14
 AC073763_0
 WPCOMMENT
 Sequence split into 4 fragments LOCUS AC073763 Accession AC073763
 Fragment Name Begin End
 AC073763_0 1 110000
 AC073763_1 100001 210000
 AC073763_2 200001 310000
 AC073763_3 300001 409770
 LOCUS AC073763 409770 bp DNA linear HTG 29-JUN-2000
 DEFINITION Mus musculus clone RP23-343P5, WORKING DRAFT SEQUENCE, 63 unordered
 pieces.
 AC073763
 AC073763.1 GI:8810380
 VERSION HTG: HTGS-PHASE1; HTGS-DRAFT.
 KEYWORDS Mus musculus.
 SOURCE Mus musculus.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS DOE Joint Genome Institute.
 TITLE Sequencing of Mouse
 JOURNAL Unpublished
 2 (bases 1 to 409770)
 REFERENCE DOE Joint Genome Institute.
 AUTHORS Direct Submission
 TITLE Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
 JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 COMMENT
 -----Genome Center
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: <http://www.jgi.doe.gov>

 Project Information
 Center Project Name: 1868949
 Center clone name: RPCI-23_343P5

 Summary Statistics
 Consensus quality: 353352 bases at least Q40
 Consensus quality: 382147 bases at least Q30
 Consensus quality: 388243 bases at least Q20
 Estimated insert size: 217190; agarose-fp estimation
 Estimated insert size: 403570; sum-of-contigs estimation
 Quality coverage: 8.5 in Q20 bases; agarose-fp estimation
 Quality coverage: 4.57 in Q20 bases; sum-of-contigs estimation.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 63 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1003: contig of 1003 bp in length
 * 1103: gap of unknown length
 * 1104: contig of 1279 bp in length
 * 2382: gap of unknown length
 * 2483: contig of 1132 bp in length


```

* 3615 3714: gap of unknown length
* 3715 4723: contig of 1009 bp in length
* 4724 4823: gap of unknown length
* 4824 6292: contig of 1469 bp in length
* 6293 6393: gap of unknown length
* 6394 7432: contig of 1039 bp in length
* 7433 7532: gap of unknown length
* 7533 8659: contig of 1338 bp in length
* 8660 8970: gap of unknown length
* 8971 10066: contig of 1097 bp in length
* 10067 10166: gap of unknown length
* 10167 11248: contig of 1082 bp in length
* 11249 13349: gap of unknown length
* 13350 13441: contig of 1993 bp in length
* 13442 14589: gap of unknown length
* 14590 14689: contig of 1148 bp in length
* 14690 15977: gap of unknown length
* 15978 15997: contig of 1108 bp in length
* 15998 16915: gap of unknown length
* 16916 17015: contig of 1018 bp in length
* 17016 18367: contig of 1352 bp in length
* 18368 18468: gap of unknown length
* 18469 19731: contig of 1264 bp in length
* 19732 19831: gap of unknown length
* 19832 20934: contig of 1103 bp in length
* 20935 22801: contig of 1767 bp in length
* 22802 22901: gap of unknown length
* 22902 24724: contig of 1822 bp in length
* 24725 24824: gap of unknown length
* 24825 26096: contig of 1272 bp in length
* 26097 26195: gap of unknown length
* 26196 27347: contig of 1152 bp in length
* 27348 27448: gap of unknown length
* 27449 29537: contig of 2090 bp in length
* 29538 29637: gap of unknown length
* 29638 31063: contig of 1426 bp in length
* 31064 31164: gap of unknown length
* 31165 33463: contig of 2200 bp in length
* 33464 36040: gap of unknown length
* 36041 36141: gap of unknown length
* 36142 38979: contig of 2839 bp in length
* 38980 42211: gap of unknown length
* 42212 42317: gap of unknown length
* 42318 44053: contig of 1736 bp in length
* 44054 44154: gap of unknown length
* 44155 45760: contig of 1607 bp in length
* 45761 45860: gap of unknown length
* 45861 48398: contig of 2538 bp in length
* 48399 52535: gap of unknown length
* 52536 56329: gap of unknown length
* 56330 56429: gap of unknown length
* 56430 60257: contig of 3828 bp in length
* 60258 60357: gap of unknown length
* 60358 63458: contig of 3101 bp in length
* 63459 66742: gap of unknown length
* 66743 66842: gap of unknown length
* 66843 69475: contig of 2633 bp in length
* 69476 69575: gap of unknown length
* 69576 73406: contig of 3831 bp in length
* 73407 73506: gap of unknown length
* 73507 77765: contig of 4259 bp in length
* 77766 77865: gap of unknown length
* 77866 82516: contig of 4651 bp in length
* 82517 82617: gap of unknown length
* 82618 88223: contig of 5507 bp in length
* 88224 88223: gap of unknown length

```

```

* 88224 93473: contig of 5250 bp in length
* 93474 95573: gap of unknown length
* 95574 98653: contig of 5080 bp in length
* 98654 98753: gap of unknown length
* 98754 103469: contig of 4716 bp in length
* 103470 103569: gap of unknown length
* 103570 109147: contig of 5578 bp in length
* 109148 109247: gap of unknown length
* 109248 116537: contig of 7290 bp in length
* 116538 124186: gap of unknown length
* 124187 124286: gap of unknown length
* 124287 132204: contig of 7918 bp in length
* 132205 132304: gap of unknown length
* 132305 140886: contig of 8582 bp in length
* 140887 140986: gap of unknown length
* 140987 151061: contig of 10075 bp in length
* 151062 151161: gap of unknown length
* 151162 159241: contig of 8080 bp in length
* 159242 159341: gap of unknown length
* 159342 167120: contig of 7779 bp in length
* 167121 167220: gap of unknown length
* 167221 178631: contig of 11411 bp in length
* 178632 178731: gap of unknown length
* 178732 190111: contig of 11380 bp in length
* 190112 190211: gap of unknown length
* 190212 201488: contig of 11277 bp in length
* 201489 201589: gap of unknown length
* 201590 212958: contig of 11370 bp in length
* 212959 227047: gap of unknown length
* 227048 227147: gap of unknown length
* 227148 241205: contig of 14058 bp in length
* 241206 241305: gap of unknown length
* 241306 258822: contig of 17517 bp in length
* 258823 258922: gap of unknown length
* 258923 277362: contig of 18340 bp in length
* 277363 277462: gap of unknown length
* 277463 299258: contig of 21896 bp in length
* 299259 299358: gap of unknown length
* 299359 321207: contig of 21849 bp in length
* 321208 321307: gap of unknown length
* 321308 342521: contig of 21214 bp in length
* 342522 342621: gap of unknown length
* 342622 374406: contig of 31785 bp in length
* 374407 409770: contig of 35264 bp in length.
* 374507 409770: contig of 35264 bp in length.

```

```

FEATURES
    Location/Qualifiers
        source
            1..409770
                /organism="Mus musculus"
                /db_xref="taxon:10090"
                /clone="RP23-343P5"
                /clone_lib="RPECI mouse BAC library 23"

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```

BASE COUNT 98446 a 106220 c 104553 g 94328 t 6223 others
ORIGIN

```

Alignment Scores:

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Pred. No.: 3 76e-49 Length: 110000
Score: 57.00 Matches: 57
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 17.38% Indels: 0
DB: 2 Gaps: 0

```

```

US-09-768-840-1 (1-328) x AC073763_0 (1-1100000)

```

```

Qy 148 ProGlyGluGluPheHisAspValGluAspAlaGluThrTyrLysLysMetLeuAlaArg 167
Db 73051 CCAGGAGAGGAGTTTCATGATGTGGAGATGCCGAGACCTACAGAGATGCTGGCTCGG 73110
Qy 168 AspGluArgArgPheArgValAlaAspClnAspGlyAspSerMetAlaThrArgGluGlu 187
Db 73111 GATGAGCGCGGATTCGCGGTAGCCGACCAAGATGGCGACTCCATGGCTACTCGGGAAGAG 73170

```


Tue May 20 14:43:22 2003

COMMENT

On Jul 11, 2002 this sequence version replaced gi:17973707.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: G1A
 Center clone name: CH230-58K9
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; Version 0.990329
 Consensus quality: 72324 bases at least Q40
 Consensus quality: 75885 bases at least Q30
 Consensus quality: 78825 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 76 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1262: contig of 1262 bp in length
 1263: gap of unknown length
 1363: contig of 1191 bp in length
 2553: gap of unknown length
 2653: gap of unknown length
 3757: contig of 1104 bp in length
 3857: gap of unknown length
 4985: contig of 1128 bp in length
 5085: gap of unknown length
 6464: contig of 1379 bp in length
 6564: gap of unknown length
 7627: contig of 1063 bp in length
 7727: gap of unknown length
 9254: contig of 1527 bp in length
 9354: gap of unknown length
 10426: contig of 1072 bp in length
 10526: gap of unknown length
 12189: contig of 1663 bp in length
 12289: gap of unknown length
 13535: contig of 1246 bp in length
 13635: gap of unknown length
 14881: contig of 1246 bp in length
 14981: gap of unknown length
 16019: contig of 1038 bp in length
 16119: gap of unknown length
 17874: contig of 1755 bp in length
 17974: gap of unknown length
 18443: contig of 1469 bp in length
 19543: gap of unknown length
 20718: contig of 1175 bp in length
 20818: gap of unknown length
 21845: contig of 1027 bp in length
 21945: gap of unknown length
 23218: contig of 1273 bp in length
 23318: gap of unknown length
 24738: contig of 1420 bp in length
 24838: gap of unknown length
 25907: contig of 1069 bp in length
 26007: gap of unknown length
 27565: contig of 1558 bp in length
 27665: gap of unknown length
 29113: contig of 1448 bp in length
 29213: gap of unknown length
 30466: contig of 1253 bp in length
 30566: gap of unknown length
 31810: contig of 1244 bp in length
 31910: gap of unknown length

Qy 188 LeuThralapheuHisProgluclupheProHisMetargAspileVal 204
 Db 73171 CTGACGGCTTCGATCGGAGAGTTCCTCACATCGGAGACATCGTG 73221

RESULT 15
 AC099450 161995 bp DNA linear HTG 12-JUL-2002
 LOCUS Rattus norvegicus clone CH230-58K9, *** SEQUENCING IN PROGRESS ***,
 DEFINITION 76 unordered pieces.

AC099450
 AC099450.3 GI:21729730
 HTG: HTGS-PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

1 (bases 1 to 161995)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
 Albrooks, S.L., Amarantunge, H.C., Are, J.R., Ayele, M., Banks, T.,
 Barbara, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
 Bouck, J., Bowie, S., Brleva, M., Brown, E., Brown, M., Bryant, N.P.,
 Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
 Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
 Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
 Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
 Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
 Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
 Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
 Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
 Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
 Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
 Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
 Hernandez, O., Hodgson, A., Hogue, M., Holloway, C., Hollins, B.,
 Homsif, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
 Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
 Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
 Kratovic, J., Kureishi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
 Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louised, H.,
 Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Martindale, A., Martinez, E.,
 Maheshwari, M., Mapua, P., Martin, R., Meador, M., Mel, G., Metzger, M.,
 Massey, E., Mawhiney, E., McLeod, M.P., Morgan, M., Morris, S.,
 Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Nguyen, N.,
 Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
 Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G.,
 Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
 Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
 Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G.,
 Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
 Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
 Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Umani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wleczyk, R., Woodson, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G., and Gibbs, R.

Direct Submission

Unpublished

2 (bases 1 to 161995)

Worley, K.C.

Direct Submission

Submitted (15-NOV-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 161995)

Worley, K.C.

Direct Submission

Submitted (12-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

* 31911	33117: contig of 1207 bp in length
* 33118	33217: gap of unknown length
* 33218	34746: contig of 1529 bp in length
* 34747	34846: gap of unknown length
* 34847	35894: contig of 1048 bp in length
* 35895	35994: gap of unknown length
* 35995	37035: contig of 1041 bp in length
* 37036	37135: gap of unknown length
* 37136	38560: contig of 1425 bp in length
* 38561	38660: gap of unknown length
* 38661	40269: contig of 1609 bp in length
* 40270	40369: gap of unknown length
* 40370	41831: contig of 1462 bp in length
* 41832	41931: gap of unknown length
* 41932	43245: contig of 1314 bp in length
* 43246	43345: gap of unknown length
* 43346	44723: contig of 1378 bp in length
* 44724	44823: gap of unknown length
* 44824	45957: contig of 1134 bp in length
* 45958	46057: gap of unknown length
* 46058	47129: contig of 1072 bp in length
* 47130	47229: gap of unknown length
* 47230	48635: contig of 1406 bp in length
* 48636	48735: gap of unknown length
* 48736	50416: contig of 1681 bp in length
* 50417	50516: gap of unknown length
* 50517	51629: contig of 1113 bp in length
* 51630	51729: gap of unknown length
* 51730	53142: contig of 1413 bp in length
* 53143	53242: gap of unknown length
* 53243	54385: contig of 1153 bp in length
* 54396	54495: gap of unknown length
* 54496	56434: contig of 1939 bp in length
* 56435	56534: gap of unknown length
* 56535	57597: contig of 1063 bp in length
* 57598	57697: gap of unknown length
* 57698	59050: contig of 1353 bp in length
* 59051	59150: gap of unknown length
* 59151	60201: contig of 1051 bp in length
* 60202	60301: gap of unknown length
* 60302	61686: contig of 1385 bp in length
* 61687	61786: gap of unknown length
* 61787	63721: contig of 1935 bp in length
* 63722	63821: gap of unknown length
* 63822	65638: contig of 1817 bp in length
* 65639	65738: gap of unknown length
* 65739	67435: contig of 1697 bp in length
* 67436	67535: gap of unknown length
* 67536	69342: contig of 1807 bp in length
* 69343	69442: gap of unknown length
* 69443	71340: contig of 1898 bp in length
* 71341	71440: gap of unknown length
* 71441	72903: contig of 1463 bp in length
* 72904	73003: gap of unknown length
* 73004	74447: contig of 1444 bp in length
* 74448	74547: gap of unknown length
* 74548	77270: contig of 2723 bp in length
* 77271	77370: gap of unknown length
* 77371	79578: contig of 2308 bp in length
* 79579	79778: gap of unknown length
* 79779	82673: contig of 2895 bp in length

Alignment Scores:

Pred. No.:	5,41e-49	Length:	161995
Score:	57.00	Matches:	57
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	17.38%	Indels:	0
DB:	2	Gaps:	0

US-09-768-840-1 (1-328) x AC099450 (1-161995)

Qy 148 ProGlyGluPheHisAspValGluAlaGluThrTyLysMetLeuAlaArg 167

Db 22144	CCAGGGGAGGANTTTCATGATGTGGAGGATGCCGAGACTTACAGAAGATGCTGGCTCGG	22203
Qy 168	AspGluArgArgPheArgValAlaAspGlnAspGlyAspSerMetAlaThrArgGluGlu	187
Db 22204	GATCAGCGCCGATTCCGGGTAGCTGACCAAGATGGGGACTCCATGGCTACTCGGGAAGAG	22263
Qy 188	LeuThrAlaPheLeuHisProGluGluPheProHisMetArgAspIleVal	204
Db 22264	CTACGGCCCTTCTGCATCTGTAGGAGATTCCCTCACAATCGGGACATCGTG	22314

Search completed: May 20, 2003, 08:33:08
Job time : 3556 secs

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GenCore version 5.1.4.p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 22:09:52 ; Search time 293 Seconds
(without alignments)
2521.008 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 328
Sequence: 1 MWRPVSLLLLLLRHCAQG.....FVGSQATNGEDLTRHDEL 328

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4368709

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters: -DB=exlhx
-Q/cgn2.1/USPTO.spool/US09768840/runat_14052003_095831_17355/app_query.fasta_1.519
-DB=N-Geneseq_101002 -QFWT=fastap -SUFFIX=olip2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFWT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09768840.ecgn.1.1.263/runat_14052003_095831_17355 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGESQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002.*

1: /SID52/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SID52/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SID52/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SID52/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SID52/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SID52/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
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14: /SID52/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
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22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	328	100.0	1055	19	Human calcium-bind
2	328	100.0	1055	22	Human calcium bind
3	328	100.0	1463	20	Human reticulocalb
4	328	100.0	1503	20	Protein PRO272 cDN
5	328	100.0	1503	21	Human PRO272 prote
6	328	100.0	1503	22	Human cDNA sequenc
7	328	100.0	1503	22	Human PRO272 cDNA
8	328	100.0	1503	22	Human anglogenesis
9	328	100.0	1542	21	cDNA encoding a bo
10	300	91.5	1507	20	Human secreted pro
11	300	91.5	1507	24	Human colon cancer
12	300	91.5	1507	24	Human colon cancer
13	300	91.5	1480	22	Human polynucleoti
14	249	75.9	1480	22	Human polynucleoti
15	249	75.9	1480	22	Human polynucleoti
16	180	54.9	1480	23	Human colon cancer
17	140	42.7	586	20	Human secreted pro
18	99	30.2	300	20	Human gene express
19	89	27.1	352	20	Human secreted pro
20	65	19.8	431	24	Human ovarian can
21	65	19.8	658	24	Human colon cancer
22	37	11.3	448	24	Human colon cancer
23	26	7.9	140	20	Human secreted pro
24	21	6.4	65	24	Human ovarian can
25	19	5.8	60	24	Rat spliced transc
26	18	5.5	408	24	Human spliced tran
27	18	5.5	411	24	Human colon cancer
28	18	5.5	501	24	Human colon tumour
29	18	5.5	2055	24	Breast cancer rela
30	18	5.5	2104	24	Human ovarian anti
31	18	5.5	2104	24	Human benign prost
32	18	5.5	2358	22	Human adenocarcino
33	17	5.2	74	22	Human cervical can
34	11	3.4	373	22	Colon tumour relat
35	11	3.4	374	22	Novel human polynu
36	10	3.0	331	22	Human secreted pro
37	10	3.0	399	21	Human 5' EST isola
38	10	3.0	399	21	Human secreted pro
39	10	3.0	550	22	Human EST-derived
40	10	3.0	569	24	Oligonucleotide fo
41	10	3.0	569	24	Oligonucleotide fo
42	10	3.0	651	19	Nucleotide sequenc
43	10	3.0	878	22	Primer specific fo
44	10	3.0	1401	19	Human T1 receptor-
45	10	3.0	1408	19	Nucleotide sequenc

ALIGNMENTS

RESULT 1
AAV57600
ID AAV57600 standard; cDNA; 1055 BP.

XX AAV57600;

XX AAV57600;

DT 15-DEC-1998 (first entry)

XX Human calcium-binding protein encoding cDNA.

KW Human; calcium-binding protein; reticulocalbin; sickle cell anaemia;
KW HCBP; beta thalassaemia; cell proliferation; cancer; adenocarcinoma;
KW Leukemia; lymphoma; melanoma; sarcoma; ss.

OS Homo sapiens.

XX Key

FT CDS Location/Qualifiers

34..1020

[illegible]

[illegible]

RESULT 5
AAC58589
ID AAC58589 standard; cDNA; 1503 BP.
XX
XX
XX
XX
DT 29-JAN-2001 (first entry)

XX	Homo sapiens.
OS	WO200104311-AI.
PN	18-JAN-2001.
XX	
PD	
XX	22-FEB-2000; 2000WO-US04414.
PF	
XX	07-JUL-1999; 99US-0143048.
PR	26-JUL-1999; 99US-0145698.
PR	28-JUL-1999; 99US-0148222.
PR	08-SEP-1999; 99WO-US20594.
PR	13-SEP-1999; 99WO-US20944.
PR	15-SEP-1999; 99WO-US21090.
PR	15-SEP-1999; 99WO-US21547.
PR	05-OCT-1999; 99WO-US23089.
PR	29-NOV-1999; 99WO-US28214.
PR	30-NOV-1999; 99WO-US28313.
PR	16-DEC-1999; 99WO-US30095.
PR	20-DEC-1999; 99WO-US30911.
PR	20-DEC-1999; 99WO-US30999.
PR	05-JAN-2000; 99WO-US00219.
XX	(GETH) GENENTECH INC.
PA	
XX	Ashkenazi AJ, Desnoyers L, Eaton DL, Ferrara N;
PI	Filvaroff EJ, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI	Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin LJ;
PI	Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI	Williams PM, Wood WI;
XX	WPI: 2001-081051/09.
DR	P-PSDB; AAB80250.
XX	Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's disease)
PT	
PT	
PT	
XX	Claim 2; Fig 79; 393pp; English.
PS	
CC	The present sequence is one of sixty one nucleic acids encoding novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. Alzheimers disease, enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum.
CC	The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.
XX	
SQ	Sequence 1503 BP; 357 A; 456 C; 474 G; 216 T; 0 other;
	Alignment Scores:
	pred. No.: 8.67e-290 Length: 1503
	Score: 328.00 Matches: 328
	Percent Similarity: 100.00% Conservative: 0
	Best local Similarity: 100.00% Mismatches: 0
	Query Match: 100.00% Indels: 0
	DB: 22 Gaps: 0
	US-09-768-840-1 (1-328) x AAF72411 (1-1503)
Qy	1 MetMetTrpArgProSerValLeuLeuLeuLeuLeuAurHisGlyAlaGlnGly 20
Db	35 ATGATGGCGGCACCATCAGTTCTGTCTTCTACTGAGGCACGCCAGGGG 94
Oy	21 LysProSerProAspAlaGlyProHisGlyGlnGlyArgValHisGlnAlaLaProLeu 40

Db 95 AAGCCATCCCAGACGCGCCCTCATGGCCAGGGAGGGTGCCACGAGGGGGCCCCCTG 154
Qy 41 SerAspAlaProHisAspAlaHisGlyAsnPheGlnTyrAspHisGluAlaPheLeu 60
Db 155 AGCGACGCTCCCATGATGACGCCACCGGAACCTTCAGTACGACCATGAGGCTTCCTG 214
Qy 61 GlyArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeu 80
Db 215 GGACGGGAAGTGGCCAGGAATTCACCACTACCCACGAGGAAAGCCAGGCCGCTG 274
Qy 81 GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerLeuAla 100
Db 275 GGGCGGATCGTGGACCGATGGACCGCGGGGACGCGCGCTGGGTGCTGGCTGGCC 334
Qy 101 GluLeuArgAlaTrpIleAlaHisThrGlnAlaArgHisIleArgAspSerValSerAla 120
Db 335 GAGCTTCGCGGTGGATCGCGCACACGCGACGCGGCGCATACGGGACATCGGTGACGCG 394
Qy 121 AlaTrpAspThrTyrAspThrAspArgAspGlyArgValGlyTrpGluGluLeuArgAsn 140
Db 395 GCCTGGGACACGTACGACACGCGACCGCGCGCGGTGGTGGGAGGAGCTGGCGAAC 454
Qy 141 AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160
Db 455 GCCACCTATGCCCACTACGCGCGCGGTGAAGAAATTCATGACGTGGAGGATGCAGAGCC 514
Qy 161 TyrIleLysMetLeuAlaArgAspGluArgArgPheArgValAlaAspGlnAspGlyAsp 180
Db 515 TACAAAAGATGTGCTCGGACGAGCGCGCTTCCGGGTGGCGACGAGGATGGGAC 574
Qy 181 SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
Db 575 TCGATGGCCACTCGAGGAGGTGACAGCCTTCCTGCACCGGAGGTTCCTCCACATG 634
Qy 201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal 220
Db 635 CGGGACATCGTGATGCTGAACCTCGGAGGACCTGGACAGAAACAAGATGGCTATGTC 694
Qy 221 GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla 240
Db 695 CAGGTGGAGGATGATCGCGATCTGTACTCAGCGGAGCCTGGGAGGAGGAGCGCGG 754
Qy 241 TrpValGlnThrGluArgGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis 260
Db 755 TGGGTGCACAGCAGGACGACGAGTCCGGGACTTCGGGATCTCGAACAAGGATGGCGAC 814
Qy 261 LeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal 280
Db 815 CTGGATGGAGTGAGTGGGCCACTGGGTGCTGCCCTGCCAGGACGAGCCCTGGTG 874
Qy 281 GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla 300
Db 875 GAAGCAACCACTGCTGCACGAGCGCACACGCAAGGATGGCGGCTGAGCAAGCG 934
Qy 301 GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp 320
Db 935 GAATCTCTGGGTAAATGGAACATCTTTGTGGCAGTCCAGGCCCACTATGCGGAGGAC 994
Qy 321 LeuThrArgHisAspGluLeu 328
Db 995 CTGACCGGGCACCATGAGTACTG 1018
RESULT 8
AAC97455
ID AAC97455 standard; cdna; 1503 BP.
XX AAC97455;
AC AAC97455;
XX
DT 28-FEB-2001 (first entry)
XX Human angiogenesis-associated protein PRO272 cdna, SEQ ID NO:112.
DE Human; angiogenesis-associated protein; PRO; endothelial cell growth;
KW

KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
KW gene therapy; transgenic animal; ss.
XX Homo sapiens.
XX WO200053753-A2.
XX 14-SEP-2000.
XX 05-JAN-2000; 2000WO-US00219.
XX 08-MAR-1999; 99WO-US05028.
XX 12-MAR-1999; 99US-0123957.
XX 14-MAY-1999; 99US-0134287.
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX 01-SEP-1999; 99WO-US20111.
XX 08-SEP-1999; 99WO-US20594.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 05-OCT-1999; 99WO-US23089.
XX 30-NOV-1999; 99WO-US28313.
XX 30-NOV-1999; 99WO-US28409.
XX 02-DEC-1999; 99WO-US28564.
XX 02-DEC-1999; 99WO-US28565.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
XX WPI; 2001-090793/10.
XX P-PSDB; AAB53085.
XX New isolated nucleic acid for producing a PRO polypeptide, analyzing
XX genetic disorders and treating cardiovascular, endothelial or
XX angiogenic disorders, such as atherosclerosis, wounds or cancer -
XX Claim 58; Fig 43; 293pp; English.
XX The invention relates to novel human angiogenesis-associated proteins
XX designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
XX PRO proteins. The invention also relates to vectors and host cells
XX comprising a PRO nucleic acid, the recombinant production of a PRO
XX protein, PRO antibodies specific for a PRO protein, fusion proteins
XX comprising a PRO protein, agonists or antagonists of a PRO protein, and
XX compounds which inhibit the expression of a PRO gene. The invention
XX additionally encompasses methods of identifying modulators of PRO
XX expression or activity; diagnosing a cardiovascular, endothelial or
XX angiogenic disorder, or a susceptibility to such a disorder by detecting
XX mutations in a PRO gene, or the expression level of a PRO gene within a
XX particular tissue; treating a cardiovascular, endothelial or angiogenic
XX disorder via the administration of a PRO protein, PRO nucleic acid, or
XX PRO agonist or antagonist; a retroviral gene therapy vector comprising a
XX cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
XX administration of a PRO protein, or an agonist or antagonist thereof.
XX PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
XX agonists and PRO antagonists may be used as therapeutic agents to treat
XX cardiovascular, endothelial or angiogenic disorders, such as
XX atherosclerosis, osteoporosis, myocardial infarction, hypertension,
XX diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
XX endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
XX disease, or stroke. PRO nucleic acids are additionally useful in the
XX recombinant production of PRO proteins, as hybridisation probes to
XX screen libraries to isolate cDNAs with sequence identity to PRO proteins,

300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753
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Qy	321	LeuThrArgHisHisAspGluLeu	328
Db	995	CTGACCCGGCACCACGATGAGCTG	1018
RESULT 9			
	AAZ36246		
TD	AAZ36246	standard:	CDNA: 1542 BP.

XX	DT	22-FEB-2000 (first entry)	
XX	DE	cDNA encoding a bone marrow secreted protein designated BMS37.	
XX	KW	Bone marrow secreted protein; bone marrow stromal cell; cytokine;	
XX	KW	cell proliferation; cell differentiation; hematopoiesis; anaemia;	
XX	KW	myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;	
XX	KW	thymic progenitor cell; colony stimulating factor; granulocyte;	
XX	KW	monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;	
XX	KW	platelet disorder; thrombocytopenia; hematopoietic stem cell;	
XX	KW	stem cell disorder; aplastic anaemia; bone differentiation;	
XX	KW	paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;	
XX	KW	ligament; nerve; wound healing; tissue repair; burn; incision; ulcer	
XX	KW	bone fracture; cartilage damage; artificial joint; ss.	
XX	OS	Homo sapiens.	
XX	FH	Key	Location/Qualifiers
XX	FT	CDS	121..1107
XX	FT		/*tag= a
XX	FT		/product= "bone marrow secreted protein"
XX	FT	sig_peptide	121..180
XX	FT		/*tag= b
XX	FT	polyA_signal	1508..1513
XX	FT		/*tag= c
XX	XX	WO9933979-A2.	
XX	PN		
XX	XX	08-JUL-1999.	
XX	PD		
XX	PF	18-DEC-1998; 98WO-US27008.	
XX	XX		
XX	PR	30-DEC-1997; 97US-0068958.	
XX	PR	24-SEP-1998; 98US-0101603.	
XX	PR	30-SEP-1998; 98US-0102540.	
XX	XX	(CHTR) CHIRON CORP.	
XX	PI		
XX	PI	Lin H, Cao L;	
XX	XX		
XX	DR	WPI; 2000-038344/03.	
XX	DR	P-PSDB; AAY53640.	
XX	XX		
XX	PT	New isolated human polynucleotide and secreted proteins can induce	
XX	PT	production of other cytokines in certain cell populations -	
XX	PS	Claim 11; Page 112-113; 120pp; English.	
XX	PS		
XX	CC	AAZ36228-49 encode bone marrow secreted proteins of human bone marrow	
XX	CC	stromal cells. The proteins can exhibit cytokine, cell proliferation	
XX	CC	cell differentiation activity (either inducing or inhibiting). They	
XX	CC	be used to support colony forming cells or factor-dependent cell li	
XX	CC	to regulate hematopoiesis, and to treat myeloid or lymphoid cell	
XX	CC	deficiencies. In addition, they may be used to support the growth a	
XX	CC		

[illegible]

Db	414	GCCTGGGACACGTACGACACGACCGCGCGTGTGGGTGGAGGAGCTGCGCAAC	473
Qy	141	AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr	160
Db	474	GCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTTCATGACGTGGAGATGCAGAGACC	533
Qy	161	TyrLysLysMetLeuAlaAraAspGluArgPheArgValAlaAspGlnAspGlyAsp	180
Db	534	TACAAAAGATGCTGGCTCGGAGACGCGGCTTCCGGGTGGCCGACACAGATGGGGAC	593
Qy	181	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
Db	594	TCGATGCCACTCGAGAGAGAGCTGACAGCCTTCTCGACCCCGAGGAGTTCCCTCACATG	653
Qy	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220
Db	654	CGGACATCGTATTGCTGAACCCCTGGAGAGACCTGGACAGAACAAAGATGGCTATGTC	713
Qy	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla	240
Db	714	CAGGTGGAGAGATACATCGCGGATCTGTACTACGCGAGCCTGGGAGGAGAGCGCGCG	773
Qy	241	TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	774	TGGGTGCAGACGAGAGACGACAGTTCGCGGACTTCCGGGATCTGAACAAGGATGGCAC	833
Qy	261	LeuAspGlySerGluValGlyHisTyrPheValLeuProProAlaGlnAspGlnProLeuVal	280
Db	834	CTGGATGGGATGGTGGTGGCCACTGGTGTCTGCCCTGCCAGGACCCCTGGTG	893
Qy	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	894	GAAGCCAAACACCTGCTGCAGARAGCGACACGACAAAGGATGGCGGCTGAGCAAGCG	953
Qy	301	Glu-IleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAs	320
Db	954	SA-AATCTGGTAAATTGGAACATGTTGTGGCAGTCAGGCCACCACTATGGYGAGGA	1012
Qy	320	pLeuThrArgHisHisAspGluLeu	328
Db	1013	CCTGACCGCGCACCATGAGCTG	1037
RESULT 11			
ID	AAL41601 standard; cdNA; 1507 BP.		
XX	AAL41601;		
AC	AAL41601;		
DT	19-APR-2002 (first entry)		
DE	Human colon cancer related coding sequence SEQ ID NO: 12.		
KW	Human; colon cancer; cytostatic; drug design; adenomatous polyp;		
KW	colorectal carcinoma; high metastatic potential colon tumour;		
KW	metastatic colon cancer; gene; ss.		
XX	Homo sapiens.		
OS	WO200196523-A2.		
PN	20-DEC-2001.		
PD	15-JUN-2001; 2001WO-US19313.		
XX	15-JUN-2000; 2000US-211835P.		
PF	(CHIR) CHIRON CORP.		
XX	Kennedy GC, Kang S, Reinhard C, Jefferson AB;		
XX	WPI; 2002-164362/21.		
DR	Detecting a cancerous colon cell, useful for diagnosing colon cancer		
PT			

Db	414	GCCTGGGACACGTACGACACGACGACGCGGTGTGGGTGGAGGAGCTGCGCAAC	473
Qy	141	AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr	160
Db	474	GCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTTCATGACGTGGAGATGCAGAGACC	533
Qy	161	TyrLysLysMetLeuAlaAraAspGluArgPheArgValAlaAspGlnAspGlyAsp	180
Db	534	TACAAAAGATGCTGGCTCGGAGACGCGGCTTCCGGGTGGCCGACACAGATGGGGAC	593
Qy	181	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
Db	594	TCGATGCCACTCGAGAGGAGCTGACAGCCCTTCCTGCACCCGAGGAGTTCCTCACCATG	653
Qy	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220
Db	654	CGGACATCGTATTGCTGAACCCCTGGAGGACCTGGACAGAACAAAGATGGCTATGTC	713
Qy	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla	240
Db	714	CAGGTGGAGGAGTACATCGCGGATCTGTACTACGCGAGCCTGGGAGGAGGACGCGCG	773
Qy	241	TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	774	TGGGTGCAGACGAGAGACGACAGTTCGCGGACTTCCGGGATCTGAACAAGGATGGCAC	833
Qy	261	LeuAspGlySerGluValGlyHisTyrPheValLeuProProAlaGlnAspGlnProLeuVal	280
Db	834	CTGGATGGGAGTGAGTGGCGCACTGGTGTCTGCCCTGCCAGGACCCCTGGTG	893
Qy	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	894	GAAGCCAAACACCTGCTGCAGARAGCGACACGACAAAGGATGGCGGCTGAGCAAGCG	953
Qy	301	Glu-IleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAs	320
Db	954	SA-AATCTGGTAAATTGGAACATGTTGTGGCAGTCAGGCCACCACTATGGYGAGGA	1012
Qy	320	pLeuThrArgHisHisAspGluLeu	328
Db	1013	CCTGACCCGCGCACCATGAGCTG	1037
RESULT 11			
ID	AAL41601 standard; cdNA; 1507 BP.		
XX	AAL41601;		
AC	AAL41601;		
DT	19-APR-2002 (first entry)		
DE	Human colon cancer related coding sequence SEQ ID NO: 12.		
KW	Human; colon cancer; cytostatic; drug design; adenomatous polyp;		
KW	colorectal carcinoma; high metastatic potential colon tumour;		
KW	metastatic colon cancer; gene; ss.		
XX	Homo sapiens.		
OS	WO200196523-A2.		
PN	20-DEC-2001.		
PD	15-JUN-2001; 2001WO-US19313.		
XX	15-JUN-2000; 2000US-211835P.		
PF	(CHIR) CHIRON CORP.		
XX	Kennedy GC, Kang S, Reinhard C, Jefferson AB;		
XX	WPI; 2002-164362/21.		
DR	Detecting a cancerous colon cell, useful for diagnosing colon cancer		
PT			

Percent Similarity:	99.39%	Conservative:	1
Best Local Similarity:	99.39%	Mismatches:	2
Query Match:	91.46%	Indels:	2
DB:	24	Gaps:	0

NO. 00-758-940-1 (1-328) X AAL41603 (1-1507)

[illegible]

1013 CCTGACCCGGCACCATGAGCTG 1037

RESULT 13
AAI63890 standard. CDNA: 1480 BP.

XX
AC
AAT63890:

XX 22-OCT-2001 (first entry)

XX
XXXXX-0000 Journal Article SEO ID NO 98.

Human; antiarthritic; antineumatic; antiproliferative; vasotropic; XX
cerebroprotective; nootropic; neuroprotective; antibacterial; virucide KW
fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; KW
neuroprotective; antiallergic; hepatotropic; antidiabetic; KW
antiinflammatory; antitumor; vulnary; anticonvulsant; antibacterial; KW
antiparasitic; cardiac; gene therapy; cancer; immune disorder; KW
cardiovascular disorder; neurological disease; infection; human; ss. KW

XX
CY

Homo sapiens.

XX
DN
W0200155308-A2.XX
8 779 3001

EXX

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PR	31-JAN-2000;	2000US-01/9063
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PR 04 - FEB - 2000; 2000US-0184664.
PR 24 - FEB - 2000; 2000US-0184664.

02-MAR-2000; 2000US-0189874;
16-MAR-2000; 2000US-0189874;
PR

17-MAR-2000; 2000US-0190076
PR 17-MAR-2000; 2000US-0198123

PR 18-APR-2000; 2000US-0205515
PR 19-MAY-2000; 2000US-0205515

PR 07-JUN-2000; 2000US-0203437
PR 07-JUN-2000; 2000US-0214886
PR 08-JUN-2000; 2000US-0214886

PR 30-JUN-2000; 2000US-0215135

07-JUL-2000; 2000US-0216880
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PR 11-JUL-2000; 2000US-0217487
PR 11-JUL-2000; 2000US-0217496
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26-JUL-2000; 2000US-0220964
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PR 14-AUG-2000; 2000US-0224519

14 - AUG - 2000; 2000US - 0225213

PR 14-AUG-2000; 2000US-0225266
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PR 14-AUG-2000; 2000US-0225268
PR 14-AUG-2000; 2000US-0225268

14-AUG-2000; 2000US-0225270

PR 14-AUG-2000; 2000US-022575

14-AUG-2000; 2000US-022575
PR 2000US-022575

PR 18-AUG-2000; 2000US-022627

PR 22-AUG-2000; 2000US-0222686

22-AUG-2000; 2000US-022718

PR 2000US-022892
23-AUG-2000;
30-AUG-2000;

PR 01-SEP-2000; 2000US-022934

01-SEP-2000; 2000US-022934

01-SEP-2000, 2000US-022950
PR
05-SEP-2000: 2000US-022950
PP

PR 05-SEP-2000; 2000US-022933

PK 06-SEP-2000; 2000US-023043

PR 08-SEP-2000; 200003 0251

PR	08-SEP-2000;	2000US-02312443
PR	08-SEP-2000;	2000US-02312444
PR	08-SEP-2000;	2000US-02314113
PR	08-SEP-2000;	2000US-02314114
PR	08-SEP-2000;	2000US-02320800
PR	08-SEP-2000;	2000US-02320801
PR	12-SEP-2000;	2000US-02319668
PR	14-SEP-2000;	2000US-02323397
PR	14-SEP-2000;	2000US-02323398
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PR	14-SEP-2000;	2000US-02324003
PR	14-SEP-2000;	2000US-02330653
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PR	21-SEP-2000;	2000US-02342274
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PR	27-SEP-2000;	2000US-02358534
PR	27-SEP-2000;	2000US-02358536
PR	29-SEP-2000;	2000US-02363237
PR	29-SEP-2000;	2000US-02363267
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PR	02-OCT-2000;	2000US-02370337
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PR	13-OCT-2000;	2000US-02399337
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PR	17-NOV-2000;	2000US-02466613
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PR	17-NOV-2000;	2000US-02492118
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PR	17-NOV-2000;	2000US-02492446
PR	17-NOV-2000;	2000US-02492445

17-NOV-2000; 2000US-0249264.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249299.
17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-0250160.
01-DEC-2000; 2000US-0250391.
03-DEC-2000; 2000US-0251030.
03-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0256719.
06-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-488781/53.
P-PSDB; AAM43584.
New isolated nucleic acids and polypeptides, useful for diagnosing,
treating and/or preventing human diseases and disorders -
Claim 1; SEQ ID NO 98; 664pp + Sequence Listing; English.
The invention relates to human polynucleotides (AAM43803-AAI64012) and
the encoded proteins (AAM434497-AAAM43660) useful for preventing, treating
or ameliorating medical conditions e.g. by protein or gene therapy. The
genes were isolated from a range of human tissues disclosed in the
specification. The nucleic acids, proteins, antibodies and (ant)agonists
are useful in the diagnosis, treatment and prevention of: (a) cancer,
e.g. breast and ovarian cancer and other cancers of the adrenal gland,
bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
urogenital; (b) immune disorders e.g. Addison's disease, allergies,
autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
colitis; (c) cardiovascular disorders such as myocardial ischaemia;
(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
and parasitic infections.
Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Sequence 1480 BP; 329 A; 458 C; 479 G; 214 T; 0 other;
Alignment Scores:
Pred. No.: 1.08e-217 Length: 1480
Score: 249.00 Matches: 327
Percent Similarity: 99.39% Conservative: 0
Best Local Similarity: 99.39% Mismatches: 1
Query Match: 75.91% Indels: 2
DB: 22 Gaps: 0
US-09-768-840-1 (1-328) x AAI63890 (1-1480)

QY	1	Met	Met	Trp	Arg	Pro	Ser	Val	Leu	Leu	Leu	Leu	Leu	Leu	Arg	His	Gly	Ala	Gln	Cly	20	
DB	47	AT	GAT	GTG	CGC	ACC	ATC	AGT	TCT	GCT	GCT	TCT	TCT	TCT	ACT	GAG	CAC	GCG	GCC	AGG	108	
QY	21	Lys	Pro	Ser	Pro	Asp	Ala	Gly	Pro	His	Gly	Gln	Gly	Arg	Val	Ile	Gln	Ala	Ala	Pro	Leu	40
DB	107	AAG	CCAT	CCCC	CAG	CGC	AGG	CCCT	CTA	TGG	CGC	AGG	GAG	GGT	GTC	ACC	AGC	GCG	CCCC	CCT	G	166
QY	41	Ser	Asp	Ala	Pro	His	Asp	Asp	Ala	His	Gly	Asn	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu	60
DB	167	ACG	GAC	GT	TCCC	ATG	ATG	ACG	CCCC	ACG	GGA	CTT	CCA	TAC	AGC	ACC	ATG	AGG	CTT	CCT	G	226

	OS	Homo sapiens.
QY	XX	61 GlyArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeu 80
Db	XX	
	PD	227 GGACGGGAAGTGGCCAAAGAAATTCGACCACACTCACCCCAGAGAAAGCCAGGCCCGCTGTG 286
QY	XX	81 GlyArgIleValAspArgMetAspArgAlaGlyAspGlyTrpValSerLeuAla 100
Db	XX	
	PD	287 GGGCGGATCGTGACCCCATATGCACCGCGGGGACGCGACGGCTGGGTGCTCGCTGGCC 346
QY	XX	101 GluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla 120
Db	XX	
	PD	347 GAGCTTCGCGCGTGGATCGGCGCACACGCACACGCGCACAATGTTCCATGCTGGAGGATGACAGACC 406
QY	XX	121 AlaTrpAspThrTyrrAspThrAspArgAspGlyArgValGlyTrpGluGluLeuArgAsn 140
Db	XX	
	PD	407 GCCTGGGACACGTACGACACGCGACGCGCGGTGCTGGTGGGAGGAGCTGCACAAC 466
QY	XX	141 AlaThrTyrrGlyHisTyrrAlaProGlyGluGluPheHisaspValGluAspAlaGluThr 160
Db	XX	
	PD	467 GCCACCTATGCCCACTACGCGCCCGGTGAAGAATTTCCATGCTGGAGGATGACAGACC 526
QY	XX	161 TyrLysLysMetLeuAlaAraGAspGluArgArgPheArgValAlaAspGlnAspGlyAsp 180
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	PD	527 TACAAAAAGATGCTGGCTCGGACAGCGCGGTTCGCGGTGGCCGACCAAGGATGGGGAC 586
QY	XX	181 SerMetalaThrArgGluGluLeuThralaPheLeuHisProGluGluPheProHisMet 200
Db	XX	
	PD	587 TCGATGGCCACTCGAGAGAGCTGACACGCTTCCTGCACCCCGAGGAGTTCCTTCACATG 646
QY	XX	201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrrVal 220
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	PD	647 CGGGACATCGTATTGCTGAACCTCGAGGACCTGGACACAAAAGATGGCTATGTC 706
QY	XX	221 GlnValGluGluTyrrIleAlaAspLeuTyrrSerAlaGluProGlyGluGluProAla 240
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	PD	707 CAGGTGGAGAGTACATCGCGATCTGTACTCAGCCGAGCTGGGGAGGAGGACCGCGC 766
QY	XX	241 TrpValGlnThrCluArgGlnGlnPheArg-AspPheArgAspLeuAsnLysAspGlyIle 260
Db	XX	
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	PD	826 CCTGGCGGAGTGGAGTGGCCACTGGGTGTGCCCCCTGCCAGGACCAAGGCGGCTGAGCAAAGC 885
QY	XX	280 lGluAlaasnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAl 300
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QY	XX	300 agluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrrGlyGluAs 320
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	PD	946 GGAATCCTGGGTAATTGGAAACATGTTGTGGGCAGTCAGGCCAACCACTATGGTAGGA 1005
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Db	XX	
	PD	1006 CCTGACCCGCGCACCATGAGCTG 1030
RESULT		14
ID		AAS31631 standard; cDNA; 1480 BP.
XX		AAS31631;
XX		(first entry)
DT		04-DEC-2001
DE		cDNA encoding novel human calcium-binding protein #55.
XX		Human; calcium-binding protein; calcium flux; neurological disease;
KW		immune dysfunction; digestive disorder; neoplastic disease;
KW		blood disorder; infectious disease; gene therapy; immunosuppressive;
KW		antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
XX		virucide; ss.
XX		

PR	27-SEP-2000;	2000US-0235834.
PR	27-SEP-2000;	2000US-0235836.
PR	27-SEP-2000;	2000US-0236327.
PR	29-SEP-2000;	2000US-0236367.
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PR	02-OCT-2000;	2000US-0236807.
PR	02-OCT-2000;	2000US-0237037.
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PR	02-OCT-2000;	2000US-0237039.
PR	13-OCT-2000;	2000US-0237040.
PR	13-OCT-2000;	2000US-0239935.
PR	20-OCT-2000;	2000US-0239937.
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PR	20-OCT-2000;	2000US-0241221.
PR	20-OCT-2000;	2000US-0241785.
PR	20-OCT-2000;	2000US-0241786.
PR	20-OCT-2000;	2000US-0241787.
PR	20-OCT-2000;	2000US-0241808.
PR	20-OCT-2000;	2000US-0241809.
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PR	08-NOV-2000;	2000US-0246610.
PR	08-NOV-2000;	2000US-0246611.
PR	17-NOV-2000;	2000US-0249207.
PR	17-NOV-2000;	2000US-0249208.
PR	17-NOV-2000;	2000US-0249209.
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PR	17-NOV-2000;	2000US-0249214.
PR	17-NOV-2000;	2000US-0249215.
PR	17-NOV-2000;	2000US-0249216.
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PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249244.
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PR	17-NOV-2000;	2000US-0249264.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	01-DEC-2000;	2000US-0250300.
PR	01-DEC-2000;	2000US-0250160.
PR	05-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
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PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	11-DEC-2000;	2000US-0251990.
PR	05-JAN-2001;	2000US-0254097.
XX		2001US-0259678.
PA	(HUMA-)	HUMAN GENOME SCING.

XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465568/50.
DR P-PSDB; AAU19946.
DR
XX
PT Isolated nucleic acid molecule encoding a calcium-binding protein is
PT used in preventing, treating or ameliorating a medical condition -
XX
PS Claim 4; SEQ ID No 65; 542pp; English.
XX
XX The present invention relates to the isolation of novel human
CC calcium-binding proteins (AAU19892-AAU19969), and cDNA and genomic
CC sequences encoding for these proteins. The sequences of the invention
CC are useful in the diagnosis, prevention and/or prognosis of diseases
CC associated with aberrant calcium flux. Such disorders include
CC neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
CC immune dysfunction (e.g. severe combined immunodeficiency, SCID),
CC digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
CC disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
CC novel calcium-binding proteins are also useful as screening tools to
CC identify antagonists and/or agonists that may enhance or inhibit
CC activities mediated by calcium-binding proteins. The polynucleotides of
CC the invention are also useful in gene therapy. AAS31577-AAS31654
CC represent cDNA sequences encoding for the novel human calcium-binding
CC proteins.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at fip.wipo.int/pub/published_pct_sequences.
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Alignment Scores:			
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[illegible]

us-09-768-840-1.olip2n.rng

Tue May 20 14:43:23 2003

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QY 181 SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
Db 587 TCGATGGCCACTCGAGAGAGCTGACAGCCTTCCTGCACCCCGAGGAGTTCCTCACAATG 646
QY 201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal 220
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QY 221 GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGluGluGluProAla 240
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RESULT 15
ABK43732
ID ABK43732 standard; cDNA: 1480 BP.
AC ABK43732;
DT 05-JUN-2002 (first entry)
DE DNA encoding novel central nervous system protein #312.
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy; gene; ss.
OS Homo sapiens.
PN WO200155318-A2.
PD 02-AUG-2001.
PF 17-JAN-2001; 2001WO-US01332.
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.

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PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
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PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
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PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
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PR 26-JUL-2000; 2000US-0220964.
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PR 14-AUG-2000; 2000US-0225213.
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PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
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PR 22-AUG-2000; 2000US-0226868.
PR 23-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 08-SEP-2000; 2000US-0231244.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
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PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
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PR 25-SEP-2000; 2000US-0234997.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
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PR 02-OCT-2000; 2000US-0237039.
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PR 13-OCT-2000; 2000US-0239937.

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Tue May 20 14:43:23 2003

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QY 221 GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla 240
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Db 1006 CCTGACCGCGCACCATGAGCTG 1030

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Search completed: May 20, 2003, 09:06:01
Job time : 326 secs

GenCore version 5.1.4_p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search; using frame_plus_p2n model

Run on: May 19, 2003, 22:09:52 ; Search time 1718 Seconds
(without alignments)
3092.037 Million cell updates/sec

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Scoring table: OLIGO

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 1

Total number of hits satisfying chosen parameters: 32308016

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DOCALIGN=200 -THR SCORE-quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
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8: em_htc:*
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17: gb_gss:*
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22: em_gss_fun:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	261	79.6	1111	14	BM920379	BM920379 AGENCOURT
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4	241	73.5	824	13	BI820206	BI820206 603037040
5	221	67.4	1103	14	BM918836	BM918836 AGENCOURT
6	207	63.1	790	12	BG775172	BG775172 602650360
7	207	63.1	1082	13	BM543703	BM543703 AGENCOURT
8	200	61.0	908	14	BQ712731	BQ712731 AGENCOURT
9	197	60.1	661	14	BM723848	BM723848 UI-P-E01-
10	197	60.1	775	12	BE875623	BE875623 601487063
11	189	57.6	681	13	BM042085	BM042085 603616096
12	176	53.7	1070	14	BM903507	BM903507 AGENCOURT
13	173	52.7	1001	9	AL550009	AL550009 AL550009
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16	149	45.4	852	9	AL543274	AL543274 AL543274
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DEFINITION	AL544155	prime, mRNA	sequence.		
ACCESSION	AL544155				
VERSION	AL544155.1	GI:12876634			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1092)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length CDNA libraries and normalization				

RESULT 3
AL543374
LOCUS

us-09-768-840-1.1.olip2n.rst

Tue May 20 14:43:24 2003

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VERSION Bi820206.1 GI:15931756
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 824)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11443 row: p column: 09
High quality sequence stop: 801.
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source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
BASE COUNT 180 a 227 c 298 g 119 t
ORIGIN

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Alignment Scores: 13e-209 Length: 824
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Score: 99.61% Conservatives: 0
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Best Local Similarity: 73.48% Indels: 1
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Qy 182 MetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMetArg 201
Db 422 ATGGCCACTCTCGAGAGGAGCTGACAGCCTTCCTGACCCCGGAGGATCCCTCATCGCG 481
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Qy 222 ValGluGluTyrlleAlaAspLeuTyrsSerAlaGluProGlyGluGluProAlaTrp 241
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Qy 262 AspGlySerGluValGlyHisTyraValLeuProAlaGlnAspGlnProLeuValGlu 281
Db 662 GATGGGAGTGGAGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 721
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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high quality sequence stop: 592.

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EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
ccode=036"
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tracking code	337 c	375 q	152 t
tracking code 036.			

Alignment Scores:	1.7e-178	Length:	1082
Pred. No.:	207.00	Matches:	220
Score:		Conservative:	0
Percent Similarity:	99.55%	Mismatches:	0
Best Local Similarity:	99.55%	Indels:	1
Query Match:	63.11%	Gaps:	0
	13		

75-00-768-840-1 (1-328) x BM543703 (1-1082)

[illegible]

RESULT /	linear	EST 20-FEB-2002
BM543703	mRNA	
LOCUS	1082 bp	
DEFINITION	AGENCOURT_6492387 NIH_MGC_125 Homo sapiens	cdna clone IMAGE:5589020
	5' .. mRNA sequence.	

ACCESSION BM543703

BM543703.1 GI:18774318

KEYWORDS EST.

SOURCE . human.

ORGANISM Homo sapiens
Eukaryota: Metazoa; Cho

Eukaryota; Mammalia; Eutheria; Pri

REFERENCE 1 (bases 1 to 1082)

AUTHORS NIH-MGC <http://mgc.ncl.nih.gov>

TITLE	National Institutes of Health
	NIH Publication No. 79-001

JOURNAL
Unpublished (1999)
Contact: Robert Straus

COMMENT:
CONTACT: ROBERT CERRASCO
Email: ccqabbs-r@email.ni

Tissue procurement: Inv

CDNA Library Preparation

cdNA Library Arrayed in

DNA sequencing by: Agencourt Bioscience Corporation
 clone distribution: MCG

clone distribution: M found through the I.M.E.

Found through the Internet
<http://image.llnl.gov>

Plate: LLAM12361 row:


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Db 371 GCCTGGACACGTACGACACGCGCGCGTGTGGTGGGAGGAGTGCACAC 430
Qy 141 AlatrThrTyGlyHisTyAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160
Db 431 GCCACCTATGCCCACTACGCGCGCGTGAAGAATTCATGACGTGGAGGATCAGAGACC 490
Qy 161 TyrLysLysMetLeuAlaAraGspGluAraGspAraGspAraGspGluAraGspGluAraGsp 180
Db 491 TACAAAAGATGCTGGCTCGGGACGAGCGCGTTCGCGGTGGCGGACACGAGTGGGAC 550
Qy 181 SerMetAlatrThrArgGluGluLeuThrAlaPheLeuHisProGluGluPhe 197
Db 551 TCGATGCCCACTCGAGAGGAGTGCACAGCTTCCTCGACCCCGAGGAGTTC 601

RESULT 11
BM042085
LOCUS BM042085
DEFINITION 603616096F1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5420806 5',
mRNA sequence.
ACCESSION BM042085
VERSION BM042085.1 GI:16771352
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 681)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1875 row: p column: 23
High quality sequence stop: 681.
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source
1. 681
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5420806"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 139 a 199 c 244 g 99 t
ORIGIN

Alignment Scores:
Pred. No.: 2,8e-162 Length: 681
Score: 189.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.62% Indels: 0
DB: 13 Gaps: 0

US-09-768-840-1 (1-328) x BM042085 (1-681)

Qy 21 LysProSerProAspAlaGlyProHisGlyGlnGlyArgValHisGlnAlaProLeu 40
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Db 115 AAGCATCCCAACGACGCGCCCTCATGCCAGGGAGGGTGCACACGCGCGCCCTG 174
Qy 41 SerAspAlaProHisAspAlaHisGlyAsnPheGlnTyrAspHisGluAlaPheLeu 60
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Db 175 AGGAGCGCTCCCATGATGACGCCACGGAACTTCCAGTACGACCATGAGGCTTCTCG 234
Qy 61 GlyArgGluValAlaValGluPheAspGlnLeuThrProGluGluSerGlnAlaAraGlu 80
Db 235 GGACGGGAAGTGGCCAGGAATTCGACCACTACCCACAGAGAAACCCAGGCCCTCTG 294
Qy 81 GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerLeuAla 100
Db 295 GGGCGGATCGTGGACCGCATGACCGCGGGGACGCGCGCTGGTGGTGGCTGGCC 354
Qy 101 GluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla 120
Db 355 GAGCTTCGCGGTGGATCGGCACACGACGACGACGACATACGGACTCGGTGAGCGCG 414
Qy 121 AlaTrpAspThrTyrAspThrAspArgAspGlyArgValGlyTrpGluGluLeuArgAsn 140
Db 415 GCCTGGGACACGTACGACACGACGCGCGCGGTGGTGGGAGGAGTGGCGAAC 474
Qy 141 AlaThrTyrGlyHisTyAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160
Db 475 GCCACCTATGCCCACTACGCGCGCGTGAAGAATTCATGACGTGGAGATCAGAGACC 534
Qy 161 TyrLysLysMetLeuAlaAraGspGluAraGspAraGspAraGspGluAraGspGluAraGsp 180
Db 535 TACAAAAGATGCTGGCTCGGGACGAGCGCGTTCGCGGTGGCGGACACGAGTGGGAC 594
Qy 181 SerMetAlatrThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
Db 595 TCGATGCCCACTCGAGAGGAGTGCACAGCTTCCTCGACCCCGAGGAGTTCCTCACATG 654
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Db 655 CGGGACATCGTATTGCTGAAACCGCTG 681

RESULT 12
BM042085
LOCUS BM042085
DEFINITION 6621943 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5721868
5', mRNA sequence.
ACCESSION BM042085
VERSION BM042085.1 GI:19352864
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1070)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM12707 row: a column: 05
High quality sequence stop: 595.
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Location/Qualifiers
1. 1070
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5721868"
/lab_host="NIH_MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;"

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Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036." 159 t 372 a

BASE COUNT	234 a	300 c	377 g	159 t
ORIGIN				
Alignment Scores:				
Pred. No.:		3.11e-150	Length:	1070
Score:	176.00		Matches:	246
Percent Similarity:	98.01%		Conservative:	3
Best Local Similarity:	98.01%		Mismatches:	5
Query Match:	35.66%		Indels:	0
	14		Gaps:	

25: 1-328) x RM903507 (1-1070)

US-09-768-840-1 (1-320)

QY	2	MettPrAproSerValLeuLeuLeuLeuLeuLeuLeuArgHisGlyAlaGlnGlyIys	21
Db	62	ATGTGGCGACCATCAGTTCTTGCTTCTGTGTACTGAGGCACGGGGCCAGGGGAAG	121
QY	22	ProSerProAspAlaGlyProHisGlyGlnGlyArgValHisGlnLaLaLapProLeuSer	41
Db	122	CCATCCCAGACGAGGCCCTCATGCCAGGGAGGGTGCACCAGCGGGCCCCCTTCAGC	181
QY	42	AspAlaProHisAspAspAlaHisGlyAsnPheGlnTyrrAspHisGluAlaPheLeuGly	61
Db	182	GACGCTCCCCATGATGACGCCACCGGCACTCCAGTAGTACGACCATGAGGCTTCCCTGGGA	241
QY	62	ArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeuGly	81
Db	242	CGGGAAGTGGCCAAGAAATTCGACCAACTCACCCACAGGAAAGCCAGGCCGCTCTGGGG	301
QY	82	ArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValserLeuAlaGlu	101
Db	302	CGGATCTGTGGCCCATGGACCGCGGGGGAGCGGCAGCGCTGGGTGCTGCTGGCCGAG	361
QY	102	LeuArGaLaTrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValserAlaAla	121
Db	362	CTTCGCGCGTGGATCGGCACACACACAGCGGCACATACGGGACTCGGGTGAGCGCGCC	421
QY	122	TrpAspThrTyrrAspThrAspArgAspGlyArgValGlyTrpGluGluLeuArgAsnAla	141
Db	422	TGGGACACCTACGACACGACGCGGCGGCGGTGTGGTGTGGAGAGGCTGCACAACGCC	481
QY	142	ThrTyrrGlyHisTyrrAlaProGlyGluGluPheHisAspValGluAspAlaGluThrTyrr	161
Db	482	ACCTATGGCCACTACCGCGCCCGTGAACAAATTTCATGACGTGGAGGATGCAGAGCTAC	541
QY	162	LysLysMetLeuAlaArgAspGluArgPheArgValLaLaAspGlnAspGly--Asps	181
Db	542	AAAAAGATGCTGCTCGGACGAGCGGGGTTCGCGGTGGCCGACCAAGGA-AT-GGGACT	599
QY	181	erMetAlaThr - ArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
Db	600	CGATGGCCATCCGAGAGGAGCTGACAGCGTTCTCTGCACCCCGAGGAGTTCCTTCACATG	659
QY	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrrVal	220
Db	660	CGGGACATCTGATTCGTGAACCCCTGGAGGACCTGGACAGAAAACAAAGATGGCTATGTC	719
QY	221	GlnValGluGluTyrrIleAlaAspLeuTyrrSerAlaGluProGlyGluGluGluProAla	240
Db	720	CAGGTGGAGGAGTACATCGCGGATCTGTACTACGCGGCCCTGGGGAGGAGGAGCCGCG	779
QY	241	TrpValGlnThrGluArgGlnGlnPhe	249
Db	780	TGGGTGCAACGGAGAGCCACGAGTTC	806

RESULT 13

AL550009 1001 bp mRNA linear EST 16-FEB-2000
LOCUS LTI_NFL006_pl2 Homo sapiens cDNA clone CS9DI053YN17 5
DEFINITION prime, mRNA sequence.
AL550009
AL550009.1 GI:12886549
EST.
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1001)
Li W.B., Gruber C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Web : www.genoscope.cns.fr.
Email: seqref@genoscope.cns.fr; Qualifiers

FEATURES source:

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Location/Qualifiers
1. 1001
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/db_xref="taxon:9606"
/clone="CSODI053N17"
/clone_lib="L1L_NFL006_PL2"
/tissue_type="placenta"
/Note="Vector: pCMVSPORT 6; Site_1: NotI;
was primed with a NotI-oligo(dT) primer.
enriched, double-stranded cDNA was digested
cloned into the Not I and Eco RV sites of
vector. Library was normalized. Library was
Life Technologies. Contact : Feng Liang Li
a division of Invitrogen 9800 Medical Cent
Rockville, Maryland 20850, USA Fax : (1) 3
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
151 t 8 others

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BASE COUNT	212 a	271 c	339 g	404 c
ORIGIN				
Alignment Scores:				
Pred. No.:		1.59e-147		1001
Score:		173.00		259
Percent Similarity:		99.23%		0
Best local Similarity:		99.23%		1
Query Match:		52.74%		2
DB:		9		0
Length:				
Matches:				
Conservative:				
Mismatches:				
Indels:				
Gaps:				

AL550009 (1-1001)

[illegible]

us-09-768-840-1.olip2n.rst

Tue May 20 14:43:24 2003

Job time : 1749 secs

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/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 142 a 278 c 291 g 197 t 1 others
ORIGIN

Alignment Scores: 2,49e-129 Length: 909
Pred. No.: 153.00 Matches: 180
Score: 98.90% Conservative: 0
Percent Similarity: 98.90% Mismatches: 1
Best Local Similarity: 46.65% Indels: 2
Query Match: 9 Gaps: 0
DB:

US-09-768-840-1 (1-328) x AL520512 (1-909)
QY 148 ProGlyGluGluPheHisAspValGluAspAlaGluThrTyrLysLysMetLeuLaarg 167
Db 904 CCCGGTGAAGAATTTCATGCGTGGAGCATGCAGAGACCTACAAAAGATGCTGCGTCGG 845
QY 168 AspGluArgArgPheArgValAla-AspGlnAspGlyAspSerMetAlaThrArgGluG1 187
Db 844 GACGAGCGGGGTTCCGGGT-GCCGCCACAGGATGGGACTCGATGCCACTCGAGAGGA 786
QY 187 uLeuthrAlaPheLeuHisProGluGluPheProHisMetArgAspIleValIleAlG1 207
Db 785 GCTGACAGCCTTCCTGCACCCCGAGAGACTCCCTCACATCGGGACATCGTGTGCTGA 726
QY 207 uThrLeuGluAspLeuAspArgAsnLysAspClyTyrValGlnValGluGluIleAl 227
Db 725 AACCTGGAGGACCTGGACAGAAACAAGATGGCTATGTCAGGTGGAGGAGTACATCGC 666
QY 227 aAspLeuTyrSerAlaGluProGlyGluGluProAlaTrpValGlnThrGluArgG1 247
Db 665 GGATCTGTACTACCGCGCCTGGGAGGAGGAGCGCGTGGTGCAGACGGAGAGGCA 606
QY 247 nGlnPheArgAspPheArgAspLeuAsnLysAspGlyHisLeuAspGlySerGluValG1 267
Db 605 GCAGTTCGGGACTTCGGGACTCTGAACAAGATGGGACCTGGATGGAGTGGAGTGGG 546
QY 267 yHisTrpValLeuProAlaGlnAspGlnProLeuValGluAlaAsnHisLeuHi 287
Db 545 CCACCTGGGTGCTGCCCTGCCAGGACACAGCCCTGGTGAAGCCCAACCACTGCTGCA 486
QY 287 sGluSerAspThrAspLysAspGlyArgLeuSerLysAlaGluIleLeuGlyAsnTrpAs 307
Db 485 CGAGAGCGACACGGACAAGATGGCGGCTGAGCANAGCGGAATCCTGGGTAATTGGAA 426
QY 307 nMetPheValGlySerGlnAlaThrAsnTyrGlyGluAspLeuThrArgHisAspG1 327
Db 425 CATGTTTGGGCGAGTCAGGCCACCACCACTATGGCGAGGACCTGACCCCGGCCACCATGA 366
QY 327 uLeu 328
Db 365 GCTG 362
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Search completed: May 20, 2003, 09:00:34

GenCore version 5.1.4_p5_4578
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OW protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 22:09:52 ; Search time 58 Seconds
(without alignments)
1734.310 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 328
Sequence: 1 MWPRSVLLLLLLRHGAQG.....FVGSQATNYGDLTRHDEL 328

Scoring table: OLIGO

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Word size: 1

Total number of hits satisfying chosen parameters: 878598

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Command line parameters:
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-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	328	100.0	1055	2	US-08-828-242-2
2	328	100.0	1055	4	US-09-206-499-2
3	328	100.0	1463	2	US-08-910-927B-2
4	328	100.0	1463	4	US-09-270-270-2
5	118	36.0	1490	4	US-09-484-970B-53
C 6	9	2.7	823	3	US-08-675-885-1
C 7	9	2.7	2160	4	US-09-588-256-1
8	9	2.7	2658	2	US-08-910-927B-4
9	9	2.7	2658	4	US-09-270-270-4
10	8	2.4	36	1	US-08-455-860-10
11	8	2.4	36	1	US-08-383-749-10
C 12	8	2.4	57	3	US-08-894-511-3

13	8	2.4	57	3	US-08-894-511-4
C 14	8	2.4	58	4	US-08-860-038-9
C 15	8	2.4	58	4	US-08-860-038-15
C 16	8	2.4	58	4	US-09-580-923-9
C 17	8	2.4	58	4	US-09-580-923-15
C 18	8	2.4	66	3	US-08-894-511-16
C 19	8	2.4	66	3	US-08-894-511-17
C 20	8	2.4	66	4	US-08-860-038-20
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C 23	8	2.4	66	4	US-09-580-923-21
C 24	8	2.4	168	1	US-08-469-802B-4
C 25	8	2.4	168	2	US-08-267-803B-4
C 26	8	2.4	171	1	US-08-469-802B-5
C 27	8	2.4	171	2	US-08-267-803B-5
C 28	8	2.4	195	1	US-08-469-802B-2
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C 30	8	2.4	201	4	US-09-018-635-32
C 31	8	2.4	210	4	US-09-134-001C-245
C 32	8	2.4	234	1	US-08-469-802B-3
C 33	8	2.4	234	2	US-08-267-803B-3
C 34	8	2.4	255	4	US-09-134-001C-242
C 35	8	2.4	270	4	US-09-146-054-8
C 36	8	2.4	270	4	US-09-664-977A-8
C 37	8	2.4	284	2	US-08-902-623-42
C 38	8	2.4	334	4	US-09-195-106-7
C 39	8	2.4	405	4	US-09-134-001C-439
C 40	8	2.4	406	4	US-09-195-106-10
C 41	8	2.4	427	4	US-08-905-223-158
C 42	8	2.4	435	4	US-09-171-209-44
C 43	8	2.4	443	4	US-08-896-164-10
C 44	8	2.4	498	4	US-09-134-001C-2491
C 45	8	2.4	506	1	US-08-469-802B-7

ALIGNMENTS

RESULT 1
US-08-828-242-2
; Sequence 2, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166

DB: 115-09-768-840-1 (1-328) x US-09-206-499-2 (1-1055)


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; NAME/KEY: CDS
; LOCATION: (1)..(2160)
US-09-588-256-1

Alignment Scores:
Pred. No.: 37.1 Length: 2160
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.74% Indels: 0
DB: 4 Gaps: 0

US-09-768-840-1 (1-328) x US-09-588-256-1 (1-2160)

QY 6 SerValLeuLeuLeuLeuLeuLeu 14
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DB 183 AGCGTGTCTGCTGCTGCTGCTGTG 157

RESULT 8
US-08-910-927B-4
; Sequence 4, Application US/08910927B
; Patent No. 5976801
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,927B
; FILING DATE: Hereewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2658 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADNOT03
; CLONE: 1601793
; US-08-910-927B-4

Alignment Scores:
Pred. No.: 45.1 Length: 2658
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 2.74% Indels: 0
DB: 2 Gaps: 0

US-09-768-840-1 (1-328) x US-08-910-927B-4 (1-2658)

QY 68 PheAspGlnLeuThrProGluGluSer 76
|||||

DB 286 TTTCATCAGCTGACACCAAGAGAGC 312
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RESULT 9

US-09-270-270-4
; Sequence 4, Application US/09270270
; Patent No. 6235477
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,270
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,927
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELEPHONE: 650-855-0355
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2658 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADN0703
; CLONE: 1601793

US-09-270-270-4

Alignment Scores:
Pred. No.: 45,1 Length: 2658
Score: 9,00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.74% Indels: 0
DB: 4 Gaps: 0

US-09-768-840-1 (1-328) x US-09-270-270-4 (1-2658)

QY 68 PheAspGlnLeuThrProGluGluSer 76
|||||

DB 286 TTTCATCAGCTGACACCAAGAGAGC 312
|||||

RESULT 10
US-08-455-860-10
; Sequence 10, Application US/08455860
; Patent No. 5686281
; GENERAL INFORMATION:
; APPLICANT: ROBERTS, MARGO R
; APPLICANT: ANDERSON, STEPHEN J
; TITLE OF INVENTION: CHIMERIC RECEPTOR MOLECULES FOR DELIVERY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CELL GENESYS, INC.
; STREET: 322 LAKESIDE DRIVE
; CITY: FOSTER CITY
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 94404

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,860
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/383,749
; FILING DATE: 03-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDEL, SARALYNN
; REGISTRATION NUMBER: 31,853
; REFERENCE/DOCKET NUMBER: CELL 19
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-9600 x 345
; TELEFAX: (415) 349-7392
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-455-860-10

Alignment Scores:
Pred. No.: 6,42 Length: 36
Score: 8,00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2,44% Indels: 0
DB: 1 Gaps: 0

US-09-768-840-1 (1-328) x US-08-455-860-10 (1-36)

QY 9 LeuLeuLeuLeuLeuArghis 16
|||||

DB 2 CTGCTCCTCTTACTCTCGGCAC 25
|||||

RESULT 11

US-08-383-749-10
; Sequence 10, Application US/08383749
; Patent No. 5712149
; GENERAL INFORMATION:
; APPLICANT: ROBERTS, MARGO R
; APPLICANT: ANDERSON, STEPHEN J
; TITLE OF INVENTION: CHIMERIC RECEPTOR MOLECULES FOR DELIVERY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CELL GENESYS, INC.
; STREET: 322 LAKESIDE DRIVE
; CITY: FOSTER CITY

Alignment Scores:
Pred. No.: 45,1 Length: 2658
Score: 9,00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.74% Indels: 0
DB: 4 Gaps: 0

FILING DATE: 23-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/00274
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST95013-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
US-08-894-511-3

Alignment Scores:

	Pred. No.:	Score:	Length:
Qy	7	9.89	57
Db	57	8.00	Matches: 8
			Conservative: 0
			Mismatches: 0
			Indels: 0
			Gaps: 0

US-09-768-840-1 (1-328) x US-08-894-511-3 (1-57)

RESULT 13

US-08-894-511-4
Sequence 4, Application US/08894511
Patent No. 6143530
GENERAL INFORMATION:
APPLICANT: CROUZET, Joel
APPLICANT: SCHERMAN, Daniel
APPLICANT: CAMERON, Beatrice
APPLICANT: WILS, Pierre
APPLICANT: DARQUET, Anne-Marie
TITLE OF INVENTION: DNA MOLECULES, PREPARATION THEREOF AND USE THEREOF IN GENE THERAPY
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/894,511
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA: FR 95/02117
APPLICATION NUMBER:
FILING DATE: 23-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/00274
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699

STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/383,749
APPLICATION NUMBER:
FILING DATE: 03-FEB-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MANDEL, SARALYNN
REGISTRATION NUMBER: 31,853
REFERENCE/DOCKET NUMBER: CELL 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 358-9600 x 345
TELEFAX: (415) 349-7392
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-383-749-10

Alignment Scores:

	Pred. No.:	Score:	Length:
Qy	9	6.42	36
Db	2	8.00	Matches: 8
			Conservative: 0
			Mismatches: 0
			Indels: 0
			Gaps: 0

US-09-768-840-1 (1-328) x US-08-383-749-10 (1-36)

RESULT 12

US-08-894-511-3/c
Sequence 3, Application US/08894511
Patent No. 6143530
GENERAL INFORMATION:
APPLICANT: CROUZET, Joel
APPLICANT: SCHERMAN, Daniel
APPLICANT: CAMERON, Beatrice
APPLICANT: WILS, Pierre
APPLICANT: DARQUET, Anne-Marie
TITLE OF INVENTION: DNA MOLECULES, PREPARATION THEREOF AND USE THEREOF IN GENE THERAPY
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/894,511
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA: FR 95/02117
APPLICATION NUMBER:


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; REFERENCE/DOCKET NUMBER: ST95013-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 57 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
US-08-894-511-4

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Alignment Scores:
Pred. No.: 9.89 Length: 57
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.44% Indels: 0
DB: 3 Gaps: 0

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US-09-768-840-1 (1-328) x US-08-894-511-4 (1-57)

```

Qy 7 ValLeuLeuLeuLeuLeuLeu 14
| | | | | | | | | | | | | | | |
Db 5 GTTCTCTCTCTCTCTCTCTCT 28

```

```

RESULT 14
US-08-860-038-9/c
; Sequence 9, Application US/08860038
; Patent No. 6287762
; GENERAL INFORMATION:
; APPLICANT: CROUZET, Joel
; APPLICANT: SCHERMAN, Daniel
; APPLICANT: WILS, Pierre
; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,038
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/15162
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR95/01468
; FILING DATE: 08-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky Esq., Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST94090-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
US-08-860-038-9
Alignment Scores:
Pred. No.: 10.1 Length: 58
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.44% Indels: 0
DB: 4 Gaps: 0

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US-09-768-840-1 (1-328) x US-08-860-038-9 (1-58)

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Qy 8 LeuLeuLeuLeuLeuLeuArg 15
| | | | | | | | | | | | | |
Db 27 CTTCTCTCTCTCTCTCTCTCG 4

```

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RESULT 15
US-08-860-038-15/c
; Sequence 15, Application US/08860038
; Patent No. 6287762
; GENERAL INFORMATION:
; APPLICANT: CROUZET, Joel
; APPLICANT: SCHERMAN, Daniel
; APPLICANT: WILS, Pierre
; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,038
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/15162
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR95/01468
; FILING DATE: 08-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky Esq., Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST94090-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
US-08-860-038-15

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Alignment Scores:
Pred. No.: 10.1 Length: 58
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0

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us-09-768-840-1.olip2n.rni

Tue May 20 14:43:23 2003

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.44% Indels: 0
DB: 4 Gaps: 0

US-09-768-840-1 (1-328) x US-08-860-038-15 (1-58)

Qy 8 LeuLeuLeuLeuLeuLeuLeuArg 15

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Db 27 CTCCTCCTCCTCCTCCTCCTCGG 4

Search completed: May 20, 2003, 08:31:14
Job time : 74 secs

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 22:09:53 ; Search time 138 Seconds
(without alignments)
3138.490 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 328
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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-Fgapext=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	328	100.0	1503	9	US-09-847-809A-2
4	328	100.0	1503	9	Sequence 2, Appli
					Sequence 220, App
					Sequence 220, App
					Sequence 220, App

5	328	100.0	1503	9	US-09-907-824-220	Sequence 220, App
6	328	100.0	1503	9	US-09-907-841-220	Sequence 220, App
7	328	100.0	1503	9	US-09-904-011-220	Sequence 220, App
8	328	100.0	1503	9	US-10-028-072-363	Sequence 220, App
9	328	100.0	1503	9	US-09-906-742-220	Sequence 220, App
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11	328	100.0	1503	9	US-10-123-904-363	Sequence 220, App
12	328	100.0	1503	9	US-10-140-470-363	Sequence 220, App
13	328	100.0	1503	9	US-09-906-838-220	Sequence 220, App
14	328	100.0	1503	9	US-09-907-613-220	Sequence 220, App
15	328	100.0	1503	9	US-08-907-942-220	Sequence 220, App
16	328	100.0	1503	9	US-10-175-746-363	Sequence 220, App
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18	328	100.0	1503	9	US-10-176-921-363	Sequence 220, App
19	328	100.0	1503	9	US-10-137-865-363	Sequence 220, App
20	328	100.0	1503	9	US-10-140-474-363	Sequence 220, App
21	328	100.0	1503	9	US-09-904-820-220	Sequence 220, App
22	328	100.0	1503	9	US-09-904-859-220	Sequence 220, App
23	328	100.0	1503	9	US-09-909-204-220	Sequence 220, App
24	328	100.0	1503	9	US-10-142-431-363	Sequence 220, App
25	328	100.0	1503	9	US-10-143-114-363	Sequence 220, App
26	328	100.0	1503	9	US-09-904-786-220	Sequence 220, App
27	328	100.0	1503	9	US-09-906-646-220	Sequence 220, App
28	328	100.0	1503	9	US-09-906-700-220	Sequence 220, App
29	328	100.0	1503	9	US-10-140-002-363	Sequence 220, App
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32	328	100.0	1503	9	US-09-903-786-220	Sequence 220, App
33	328	100.0	1503	9	US-10-142-419-363	Sequence 220, App
34	328	100.0	1503	9	US-09-902-736-220	Sequence 220, App
35	328	100.0	1503	9	US-09-904-119-220	Sequence 220, App
36	328	100.0	1503	9	US-09-904-956-220	Sequence 220, App
37	328	100.0	1503	9	US-09-907-794-220	Sequence 220, App
38	328	100.0	1503	9	US-10-123-262-363	Sequence 220, App
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45	328	100.0	1503	9	US-09-907-925-220	Sequence 220, App

ALIGNMENTS

RESULT 1
US-09-768-840-2
; Sequence 2, Application US/09768840
; Patent No. US20010012831A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/768,840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/206,499

CLONE: 922578
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-847-809A-2

Alignment Scores.

Pred. No.:	0	Length:	1463
Score:	328.00	Matches:	328
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-768-840-1 (1-328) x US-09-847-809A-2 (1-1463)

[illegible]

RESULT.T 3

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US-09-905-291A-220
: Sequence 220, Application US/09905291A
: Patent No. US20020160374A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Flivaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gertlisen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transferred
: TITLE OF INVENTION: Acids Encoding the
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/905/291A
: PRIOR APPLICATION NUMBER: PCT/US00/0444
: PRIOR FILING DATE: 2001-07-12
: PRIOR APPLICATION NUMBER: PCT/US00/0444
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/2059
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/2094
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/2109
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/2154
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/2308
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/2821
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/2831
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/2856
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/2856
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/3009
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/3091
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/3099

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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 220
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-505-291A-220

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Alignment Scores:			
Pred. No.:	0	Length:	1503
Score:	328.00	Matches:	328
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US 00-769-840-1 (1-328) x US-09-905-291A-220 (1-1503)

[illegible]

Db	815	CTGGATGGGAGTCTGAGTGGGCCACTGGGTGCTGCCCCCTGCCACGAGCAGCCCTGGTG	876
QY	281	GLuAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	875	GAAGCCCAACCACTGCTGCACGAGAGCGACCGACCAAGGATGGCGGCTGAGCAAAGCG	934
QY	301	GLuIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTrpGlyGluAsp	320
Db	935	GAATATCTGGGTATTGGAACATGTTTGTGGCAGTCAGGCCACCACTATGCGGAGGAC	994
QY	321	LeuThrArgHisHisAspGluLeu	328
Db	995	CTGACCCGGCCACCAAGATGAGCTG	1018
RESULT 4			
US-09-902-853-220			
; Sequence 220, Application US/09902853			
; Publication No. US20020192659A1			
; GENERAL INFORMATION:			
; APPLICANT: Genentech, Inc.			
; APPLICANT: Ashkenazi, Avi			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, A.			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, Christopher J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth, J.			
; APPLICANT: Kljavin, Ivar J.			
; APPLICANT: Mather, Jennie P.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William, I.			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucle			
; TITLE OF INVENTION: Acids Encoding the Same			
; FILE REFERENCE: 10466-14			
; CURRENT APPLICATION NUMBER: US/09/902,853			
; CURRENT FILING DATE: 2001-07-10			
; PRIOR APPLICATION NUMBER: US/09/665,350			
; PRIOR FILING DATE: 2000-09-18			
; PRIOR APPLICATION NUMBER: US 60/143,048			
; PRIOR FILING DATE: 1999-07-07			
; PRIOR APPLICATION NUMBER: US 60/145,698			
; PRIOR FILING DATE: 1999-07-26			
; PRIOR APPLICATION NUMBER: US 60/146,222			
; PRIOR FILING DATE: 1999-07-28			
; PRIOR APPLICATION NUMBER: PCT/US99/20594			
; PRIOR FILING DATE: 1999-09-08			
; PRIOR APPLICATION NUMBER: PCT/US99/20944			
; PRIOR FILING DATE: 1999-09-13			
; PRIOR APPLICATION NUMBER: PCT/US99/21090			
; PRIOR FILING DATE: 1999-09-15			
; PRIOR APPLICATION NUMBER: PCT/US99/21547			
; PRIOR FILING DATE: 1999-09-15			
; PRIOR APPLICATION NUMBER: PCT/US99/23089			
; PRIOR FILING DATE: 1999-10-05			
; PRIOR APPLICATION NUMBER: PCT/US99/28214			
; PRIOR FILING DATE: 1999-11-29			
; PRIOR APPLICATION NUMBER: PCT/US99/28313			
; PRIOR FILING DATE: 1999-11-30			
; PRIOR APPLICATION NUMBER: PCT/US99/28564			

APPLICANT: WILLIAM, I.
 APPLICANT: Wood, William, I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: 10466-14

FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
CURRENT PCT NUMBER: US/09/665,350
PRIOR APPLICATION NUMBER: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564

[illegible]


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: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: REMAINING PRIOR Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 220
: LENGTH: 1503
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-907-841-220

Alignment Scores:
Pred. No.: 0
Score: 328.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 9
Length: 1503
Matches: 328
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

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[illegible]

RESULT 8

US 10-028-072-363 Application US/10028072

Sequence 363 Publication No. US20030004311A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: Desoyers, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang

TITLE OF INVENTION:

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/028,072

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

[illegible]

1	PRIOR FILING DATE:	1998-06-17
2	PRIOR APPLICATION NUMBER:	60/089907
3	PRIOR FILING DATE:	1998-06-18
4	PRIOR APPLICATION NUMBER:	60/089947
5	PRIOR FILING DATE:	1998-06-19
6	PRIOR APPLICATION NUMBER:	60/090344
7	PRIOR FILING DATE:	1998-06-23
8	PRIOR APPLICATION NUMBER:	60/090429
9	PRIOR FILING DATE:	1998-06-24
10	PRIOR APPLICATION NUMBER:	60/090445
11	PRIOR FILING DATE:	1998-06-24
12	PRIOR APPLICATION NUMBER:	60/090538
13	PRIOR FILING DATE:	1998-06-24
14	PRIOR APPLICATION NUMBER:	60/090863
15	PRIOR FILING DATE:	1998-06-26
16	PRIOR APPLICATION NUMBER:	60/091360
17	PRIOR FILING DATE:	1998-07-01
18	PRIOR APPLICATION NUMBER:	60/091519
19	PRIOR FILING DATE:	1998-07-02
20	PRIOR APPLICATION NUMBER:	60/091982
21	PRIOR FILING DATE:	1998-07-07

Alignment Scores:			
Pred. No.:	0	Length:	1503
Score:	328.00	Matches:	328
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	9	Gaps:	0

ПС-09-768-840-1 (1-328) x US-10-028-072-363 (1-1503)

QY	1	Met	Met	Trp	Arg	Pro	Ser	Val	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	His	Gly	Ala	Gln	Gly	20
Db	35	AT	GAT	G	TG	CG	AC	CA	T	C	A	G	T	T	C	T	G	T	C	T	G	94
QY	21	Lys	Pro	Ser	Pro	Asp	Ala	Gly	Pro	His	Gly	Gln	Gly	Arg	Val	His	Gln	Ala	Ala	Pro	Leu	40
Db	95	A	G	C	C	A	T	C	C	C	A	G	C	C	T	A	T	G	C	C	A	154
QY	41	Ser	Asp	Ala	Pro	His	Asp	Asp	Ala	His	Gly	Asn	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu	60
Db	155	A	G	C	A	C	G	C	T	C	C	C	A	T	G	A	T	C	C	C	A	214
QY	61	Gly	Arg	Glu	Val	Ala	Lys	Glu	Phe	Asp	Gln	Leu	Thr	Pro	Glu	Glu	Ser	Gln	Ala	Arg	Leu	80
Db	215	G	A	C	G	G	A	A	T	G	C	A	A	C	T	C	A	C	C	A	G	274
QY	81	Gly	Arg	Ile	Val	Asp	Arg	Met	Asp	Arg	Ala	Gly	Asp	Gly	Asp	Gly	Trp	Val	Ser	Leu	Ala	100
Db	275	G	G	C	G	G	A	T	G	T	G	A	C	C	G	C	G	G	G	A	C	334
QY	101	Glu	Leu	Arg	Ala	Thr	Ile	Ala	His	Thr	Gln	Arg	His	Ile	Arg	Asp	Ser	Val	Ser	Ala	120	
Db	335	G	A	S	C	T	T	C	G	C	G	T	G	A	T	C	A	T	C	G	394	
QY	121	Ala	Trp	Asp	Thr	Tyr	Asp	Thr	Asp	Arg	Asp	Gly	Arg	Val	Gly	Trp	Glu	Leu	Arg	Asn	140	
Db	395	G	C	T	G	G	A	C	A	G	T	G	A	C	C	G	G	T	G	G	454	
QY	141	Ala	Thr	Tyr	Gly	His	Tyr	Ala	Pro	Gly	Glu	Phe	His	Asp	Val	Glu	Asp	Ala	Glu	Thr	160	
Db	455	G	C	A	C	C	T	A	T	G	C	C	C	G	T	G	A	A	T	T	514	
QY	161	Tyr	Lys	Ser	Met	Leu	Ala	Arg	Asp	Clu	Arg	Phe	Arg	Val	Ala	Asp	Gln	Asp	Gly	Asp	180	
Db	515	T	A	C	A	A	A	A	G	A	T	G	C	T	G	G	A	C	C	G	574	
QY	181	Ser	Met	Ala	Thr	Arg	Glu	Leu	Thr	Ala	Phe	Leu	His	Pro	Glu	Glu	Phe	Pro	His	Met	200	
Db	575	T	C	G	A	T	G	C	C	A	T	G	C	C	C	C	C	C	C	C	634	
QY	201	Arg	Asp	Ile	Val	Ile	Ala	Glu	Thr	Leu	Glu	Asp	Leu	Asp	Arg	Asn	Lys	Asp	Gly	Tyr	Val	220

D	b	635	CGGACATCTGATTGCTGAAACCTTGGAGGACCTGGACAGAAAACAAAGATGGCTATGTC	594
Q	y	221	GlnValGluGlnTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla	240
D	b	695	CAGTGGAGGAGTACATCGCGGATCTGTACTAGCCGAGCCTTGGGAGGAGGAGCGCGC	754
Q	y	241	TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
D	b	755	TGGTGGCAGCGGAGAGCGACAGCTCCGGGACTTCGGGATCTGAACAAGATGGGCAC	814
Q	y	261	LeuAspGlySerGluValGlyHisTrpValLeuProAlaGlnAspGlnProLeuVal	280
D	b	815	CTGGATGGAGTGGAGTGGGGCACTGGGTGCTGCCCTGCCCGACGACCCTGGTG	874
Q	y	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
D	b	875	GAAGCGCAACCACTGCTGCACGAGAGGCACACGACAAAGATGGCGGCTGAGCAAAAGC	934
Q	y	301	GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
D	b	935	GAATCTCTGGGTAATTGGAACATGTTTGTGGCGAGTCAGGCCACCACTATGGCGAGGAC	994
Q	y	321	LeuThrArgHisHisAspGluLeu	328
D	b	995	CTGACCGGCACACCATGAGCTG	1018

RESULT 9
HS-09-906-742-220

US-09-906-742-220
; Sequence 220, Application US/09906742
; Sequence 220, Application US20030023054A1

Publication No. US20

7 GENERAL INFORMATION:
7
7 APPLICANT: Genentech, Inc.
7 APPLICANT: Ashkenazi, Avi
7 APPLICANT: Botstein, David
7 APPLICANT: Desnoyers, Luc
7 APPLICANT: Eaton, Dan L.
7 APPLICANT: Ferrara, Napoleone
7 APPLICANT: Filvaroff, Ellen
7 APPLICANT: Gong, Sherman
7 APPLICANT: Gao, Wei-Olang
7 APPLICANT: Gerber, Hanspeter
7 APPLICANT: Gerritsen, Mary E.
7 APPLICANT: Goddard, A.
7 APPLICANT: Godowski, Paul J.
7 APPLICANT: Grimaldi, Christopher J.
7 APPLICANT: Gurney, Austin L.
7 APPLICANT: Hillan, Kenneth, J.
7 APPLICANT: Kljavin, Ivar J.
7 APPLICANT: Mather, Jennie P.
7 APPLICANT: Pan, James
7 APPLICANT: Paoni, Nicholas F.
7 APPLICANT: Roy, Margaret Ann
7 APPLICANT: Stewart, Timothy A.
7 APPLICANT: Tumas, Daniel
7 APPLICANT: Williams, P. Mickey
7 APPLICANT: Wood, William, I.
7
7 TITLE OF INVENTION: Acids Encoding and Tri
7
7 FILE REFERENCE: 10466-14
7
7 CURRENT APPLICATION NUMBER: US/09/99-16
7 CURRENT FILING DATE: 2001-07-16
7
7 PRIOR APPLICATION NUMBER: 09/665,352
7 PRIOR FILING DATE: 2000-09-18
7
7 PRIOR APPLICATION NUMBER: PCT/US00/0
7 PRIOR FILING DATE: 2000-02-22
7
7 PRIOR APPLICATION NUMBER: US 60/14
7 PRIOR FILING DATE: 1999-07-07
7
7 PRIOR APPLICATION NUMBER: US 60/14
7 PRIOR FILING DATE: 1999-07-26
7
7 PRIOR APPLICATION NUMBER: US 60/14
7 PRIOR FILING DATE: 1999-07-28
7
7 PRIOR APPLICATION NUMBER: PCT/US99

```
; APPLICANT: Williams, P. Mickey
;
; APPLICANT: Wood, William, I.
;
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
```



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Oy 121 AlaTrpAspThrTyrAspThrAspArgAspGlyArgValGlyTrpGluLeuLeuArgAsn 140
Db 395 GCCTGGGACACGTACACGACCGGCGCGGCGGTGGTGGGAGGAGCTGGCGAAC 454
Oy 141 AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160
Db 455 GCCACCTATGGCCACTACGCGCGGCGGTGAAGAAATTCATGACGTGGAGGATGCCAGACC 514
Oy 161 TyrLysMetLeuAlaArgAspGluArgArgPheArgValAlaAspGlnAspGlyAsp 180
Db 515 TACAAAAGATGCTGGCTGGGACGAGCGGCGTTTCGGGTGGCGGACGAGATGGGAC 574
Oy 181 SerMetAlaThrArgGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
Db 575 TCGATGGCCACTCGAGAGAGCTGACAGCCTTCCTGCACCCCGAGGAGTCCCTTCACATG 634
Oy 201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal 220
Db 635 CGGGACATCGTGATGCTGAAACCTCGGAGGACCTGGACAGAAACAAAGATGGCTATGTC 694
Oy 221 GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla 240
Db 695 CAGGTGGAGGAGTACATCGCGGATCTGACTCAGCCGAGCCTGGGAGGAGGAGCGCGG 754
Oy 241 TrpValGlnThrGluArgGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis 260
Db 755 TGGGTGCAGACGAGAGCGACAGTCCGGGACTTCGGGATCTGAACAAGATGGGCAC 814
Oy 261 LeuAspGlySerGluValGlyHisTrpValLeuProAlaGlnAspGlnProLeuVal 280
Db 815 CTGATGGGAGTGGTGGGCCACTGGTCTGCCCTGCCAGGACCGCCCTGGTG 874
Oy 281 GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla 300
Db 875 GAAGCCACCACTGCTGCAGGAGCGACGACGACGACGACGACGACGACGACGACGACG 934
Oy 301 GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp 320
Db 935 GAATCTCTGGGTAAATGGAAACATGTTGTGGCAGTCAGGCCACCACTATGGGAGAG 994
Oy 321 LeuThrArgHisHisAspGluLeu 328
Db 995 CTGACCCGCGACACGATGAGCTG 1018

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RESULT 12

US-10-140-470-363

Sequence 363, Application US/10140470

Publication No. US20030022331A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Naureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C160

CURRENT APPLICATION NUMBER: US/10/140,470

CURRENT FILING DATE: 2002-05-06

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

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; SEQ ID NO 363
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-470-363

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Alignment Scores:

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Pred. No.: 0 Length: 1503
Score: 328.00 Matches: 328
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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US-09-768-840-1 (1-328) x US-10-140-470-363 (1-1503)

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Oy 1 MetMetTrpArgProSerValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 20
Db 35 ATGATGTGGCGACCATCAGTTCTGCTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 94
Oy 21 LysProSerProAspAlaGlyProHisGlyGlnGlyArgValHisGlnAlaAlaProLeu 40
Db 95 AAGCCATCCCGACAGCAGCGCCCTCATGGCCAGGGAGGTGCACCCAGCGGCCCCCTG 154
Oy 41 SerAspAlaProHisAspAlaHisGlyAsnPheGlnTyrAspHisGlnAlaPheLeu 60
Db 155 AGGCACGCTCCCATGATGACGCCCGCCAGCGGAACTTCCAGTACGACCATGAGGCTTTCT 214
Oy 61 GlyArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeu 80
Db 215 GGACGGGAGTGGCCAAAGAAATTCGACCAACTCACCCAGAGGAAAGCCAGGCCGCTG 274
Oy 81 GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerLeuAla 100
Db 275 GGCGGATCGTGACCGCATGACCGCGCGGGGAGCGGCGCGGTGGTGGTGGTGGTGGTGG 334
Oy 101 GluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla 120
Db 335 GAGCTTGGCGGTGTGATCGGCACACGCGCAGCGGACATACCGGACATACCGGACATAC 394
Oy 121 AlaTrpAspThrTyrAspThrAspArgAspGlyArgValGlyTrpGluGluLeuArgAsn 140
Db 395 GCCTGGGACACGTACGACACGCGCGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 454
Oy 141 AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160
Db 455 GCCACCTATGGCCACTACGCGCGCGGTGAAGAAATTCATGACGTGGAGGATGCCAGACC 514
Oy 161 TyrLysLysMetLeuAlaArgAspGluArgArgPheArgValAlaAspGlnAspGlyAsp 180
Db 515 TACAAAAGATGCTGGCTGGGACGAGCGCGGTTCGGGTGGCGGACCAAGATGGGAC 574
Oy 181 SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
Db 575 TCGATGGCCACTCGAGAGGAGCTGACACGCTTCTCACCACCGGAGGATCCCTCATGAT 634
Oy 201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal 220
Db 635 CGGGACATCGTGATGCTGAACCCCTGGAGGACCTGGACAGAAACAAAGATGGCTATGTC 694
Oy 221 GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla 240
Db 695 CAGGTGGAGGAGTACATCGCGGATCTGACTCAGCGGACCTGGGAGGAGGAGGAGGAGG 754
Oy 241 TrpValGlnThrGluArgGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis 260
Db 755 TGGGTGCAGACGAGAGCGAGCTTCGGGACTTCCGGGATCTGAACAAGATGGGCAC 814
Oy 261 LeuAspGlySerGluValGlyHisTrpValLeuProAlaGlnAspGlnProLeuVal 280
Db 815 CTGATGGGAGTGGTGGGCCACTGGTCTGCCCTGCCAGGACCGCCCTGGTG 874
Oy 281 GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla 300

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QY	241	TtpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	755	TGGGTGCACAGCAGCAGCAGCAGCAGTCCGGGACTTCGGGGATCTGACCAAGATGGGCAC	814
QY	261	LeuAspGlySerGluValGlyHisTrpValLeuProPheGlnGlnAspGlnProLeuVal	280
Db	815	CTGGATGGCAGTGAAGTGGGCCACTGGGTCTGCCCTGCCAGGACCAGCCCTGGTG	874
QY	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	875	GAAGCCAAACCACCTGCTGCACGAGCGACGCGAAGGATGGCGCGCTGACCAAGCG	934
QY	301	GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
Db	935	GAATCTCTGGGTANTTGGAAACATGTTTGTGGCCAGTCCAGCCACCAACTATGCGAGGAC	994
QY	321	LeuThrArgHisHisAspGluLeu	328
Db	995	CTGACCCGGCCACCAGATGAGCTG	1018

RESULT 14

US-09-907-613-220
; Sequence 220, Application US/09907613
; Publication No. US20030027145A1

GENERAL INFORMATION:

1	APPLICANT:	Genentech, Inc.	CURRENT APPLICATION NUMBER:	US/09/907
2	APPLICANT:	Ashtenazi, Inc.	CURRENT FILING DATE:	2001-07-17
3	APPLICANT:	Botstein, David	PRIOR APPLICATION NUMBER:	PCT/US00/040
4	APPLICANT:	Desnoyers, Luc	PRIOR FILING DATE:	2000-02-22
5	APPLICANT:	Eaton, Dan L.	PRIOR APPLICATION NUMBER:	US 60/143,0
6	APPLICANT:	Ferrata, Napoleone	PRIOR FILING DATE:	1999-07-07
7	APPLICANT:	Filivartoff, Ellen	PRIOR APPLICATION NUMBER:	US 60/145,6
8	APPLICANT:	Fong, Sherman	PRIOR FILING DATE:	1999-07-26
9	APPLICANT:	Gao, Wei-Qiang	PRIOR APPLICATION NUMBER:	US 60/146,2
10	APPLICANT:	Gerber, Hanspeter	PRIOR FILING DATE:	1999-07-28
11	APPLICANT:	Gerritsen, Mary E.	PRIOR APPLICATION NUMBER:	PCT/US99/20
12	APPLICANT:	Goddard, A.	PRIOR FILING DATE:	1999-09-08
13	APPLICANT:	Godowski, Paul J.	PRIOR APPLICATION NUMBER:	PCT/US99/20
14	APPLICANT:	Grimaldi, Christopher J.	PRIOR FILING DATE:	1999-09-13
15	APPLICANT:	Gurney, Austin L.	PRIOR APPLICATION NUMBER:	PCT/US99/21
16	APPLICANT:	Hillan, Kenneth, J.	PRIOR FILING DATE:	1999-09-15
17	APPLICANT:	Kljavin, Ivar J.	PRIOR APPLICATION NUMBER:	PCT/US99/21
18	APPLICANT:	Mather, Jennie P.	PRIOR FILING DATE:	1999-09-15
19	APPLICANT:	Pan, James	PRIOR APPLICATION NUMBER:	PCT/US99/23
20	APPLICANT:	Paoni, Nicholas F.		
21	APPLICANT:	Roy, Margaret Ann		
22	APPLICANT:	Stewart, Timothy A.		
23	APPLICANT:	Tumas, Daniel		
24	APPLICANT:	Williams, P. Mickey		
25	APPLICANT:	Wood, William, I.		
26	TITLE OF INVENTION:	Secreted and Trans		
27	TITLE OF INVENTION:	Acids Encoding t		
28	FILE REFERENCE:	10466-14		
29	CURRENT APPLICATION NUMBER:	US/09/907		
30	CURRENT FILING DATE:	2001-07-17		
31	PRIOR APPLICATION NUMBER:	PCT/US00/040		
32	PRIOR FILING DATE:	2000-02-22		
33	PRIOR APPLICATION NUMBER:	US 60/143,0		
34	PRIOR FILING DATE:	1999-07-07		
35	PRIOR APPLICATION NUMBER:	US 60/145,6		
36	PRIOR FILING DATE:	1999-07-26		
37	PRIOR APPLICATION NUMBER:	US 60/146,2		
38	PRIOR FILING DATE:	1999-07-28		
39	PRIOR APPLICATION NUMBER:	PCT/US99/20		
40	PRIOR FILING DATE:	1999-09-08		
41	PRIOR APPLICATION NUMBER:	PCT/US99/20		
42	PRIOR FILING DATE:	1999-09-13		
43	PRIOR APPLICATION NUMBER:	PCT/US99/21		
44	PRIOR FILING DATE:	1999-09-15		
45	PRIOR APPLICATION NUMBER:	PCT/US99/21		
46	PRIOR FILING DATE:	1999-09-15		
47	PRIOR APPLICATION NUMBER:	PCT/US99/23		

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1  PRIOR FILING DATE: 1999-10-05
2  PRIOR APPLICATION NUMBER: PCT/US99/28214
3  PRIOR FILING DATE: 1999-11-29
4  PRIOR APPLICATION NUMBER: PCT/US99/28313
5  PRIOR FILING DATE: 1999-11-30
6  PRIOR APPLICATION NUMBER: PCT/US99/28564
7  PRIOR FILING DATE: 1999-12-02
8  PRIOR APPLICATION NUMBER: PCT/US99/28565
9  PRIOR FILING DATE: 1999-12-02
10 PRIOR APPLICATION NUMBER: PCT/US99/30095
11 PRIOR FILING DATE: 1999-12-16
12 PRIOR APPLICATION NUMBER: PCT/US99/30911
13 PRIOR FILING DATE: 1999-12-20
14 PRIOR APPLICATION NUMBER: PCT/US99/30999
15 PRIOR FILING DATE: 1999-12-20
16 PRIOR APPLICATION NUMBER: PCT/US00/00219
17 PRIOR FILING DATE: 2000-01-05
18 NUMBER OF SEQ ID NOS: 423
19 SEQ ID NO 220
20 LENGTH: 1503
21 TYPE: DNA
22 ORGANISM: Homo sapiens
23 US-09-907-613-220

Alignment Scores:
Pred. No.: 0
Score: 328.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Gaps: 0
Matches: 328
Length: 1503
Conservative: 0
Mismatch: 0
Indel: 0
Gap: 0

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US-09-768-840-1 (1-328) x US-09-907-613-220 (1-1503)

Alignment Scores:

[illegible]

201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal 220
 |||||
 635 CGGGACATCGTGATTGCTGAACCTCGAGGACCTGGACAAACAAAGATGCTATGTC 694
 |||||
 221 GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla 240
 |||||
 695 CAGGTGGAGGACTACATCGCGATCTGTACTCAGCCGAGGCTGGGGAGGAGGACCGCG 754
 |||||
 241 TrpValGlnThrGluArgGlnClnPheArgAspPheArgAspLeuAsnLysAspGlyHis 260
 |||||
 755 TGGGTCCACACGAGGAGGAGCGAGCGTCCGGGACATCCGGGATCTGAACAAGGATGGGCAC 814
 |||||
 261 LeuAspGlySerGluValGlyHisTrpValLeuProAlaGlnAspGlnProLeuVal 280
 |||||
 815 CTGGATGGGAGTGAGTGGGCCACTGGGTGCTGGCCCTGCCAGGACACCCCTGGTG 874
 |||||
 281 GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla 300
 |||||
 875 GAAGCCCAACCACTGCTGCACGAGCGGACGACGACAGGATGGCGGCTGAGCAAAAGCG 934
 |||||
 301 GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp 320
 |||||
 935 GAAATCTCGTAAATGGAACATGTTTGTGGCGAGTCAGGCCACCACTATGCGGAGGAC 994
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 321 LeuThrArgHisAspGluLeu 328
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 995 CTGACCCCGGACACGATGAGCTG 1018
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 RESULT 15
 US-09-907-942-220
 ; Sequence 220, Application US/09907942
 ; Publication No. US20030027146A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gottard, Mary E.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paonl, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/907, 942
 ; CURRENT FILING DATE: 2002-01-22
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594

QY 161 TyrLysLysMetLeuAlaArgAspGluArgArgPheArgValAlaAspGlnAspGlyAsp 180
 Db 515 TACAAAAGATGCTGGCTCGGAGCAGCGCGTTCCGGGTGGCCGACCCAGGATGGGAC 574
 QY 181 SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
 Db 575 TCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCCTGCACCCCGAGGAGTTCCCTCACATG 634
 QY 201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal 220
 Db 635 CGGGACATCGTGAATGCTGAAACCCCTGGAGGACCTGGACAGAAACAAGATGGCTATGTC 694
 QY 221 GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla 240
 Db 695 CAGGTGGAGGAGTACATCGCGATCTGTACTCAGCCGAGCCCTGGGGAGGAGGCCGCG 754
 QY 241 TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis 260
 Db 755 TGGGTGCAGACGAGGAGCGCAGCTTCGGGACTTCGGGATCTGAACAAGGATGGGCAC 814
 QY 261 LeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal 280
 Db 815 CTGGATGGGAGTGAGTGGGCCACTGGGTGCTGCCCTGCCAGGACAGCCCTGGTG 874
 QY 281 GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla 300
 Db 875 GAAGCCAACCACTGCTGCACGAGAGCGCACACGACAGGATGGCGGCTGAGCAAAGCG 934
 QY 301 GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp 320
 Db 935 GAAATCCCTGGGTAATTTGGAACATGTTTGTGGGCAGTCAGGCCCACTATATGGCGAGGAC 994
 QY 321 LeuThrArgHisHisAspGluLeu 328
 Db 995 CTGACCCGGCACCAGGATGAGCTG 1018

Search completed: May 20, 2003, 09:50:38
 Job time : 170 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2003, 10:34:22 ; Search time 1.10557 Seconds
(without alignments)
487.704 Million cell updates/sec

Title: US-09-768-840-1_COPY_254_266
Perfect score: 70
Sequence: 1 DLNKGHLGSEV 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	48	68.6	325	1 RCN1_MOUSE	Q05186 mus musculus
2	48	68.6	325	1 RCN1_MOUSE	Q15293 homo sapien
3	47	67.1	753	1 PPE2_HUMAN	O14830 homo sapien
4	47	67.1	757	1 PPE2_MOUSE	O35385 mus musculus
5	44	62.9	1628	1 NAGH_CLOPE	P26831 clostridium
6	43	61.4	653	1 PPE1_HUMAN	O14829 homo sapien
7	43	61.4	662	1 YAE8_MOUSE	P39722 saccharomyc
8	43	61.4	1638	1 ITN2_MOUSE	Q920r6 mus musculus
9	43	61.4	1696	1 ITN2_HUMAN	Q920r3 homo sapien
10	42	60.0	249	1 HIS4_PASMU	O9clm1 pasteurilla
11	41	58.6	207	1 CB23_TETTH	P20473 tetrahymena
12	41	58.6	587	1 CMG3_CAEEL	Q19529 caenorhabdi
13	40	57.1	102	1 S111_RABIT	P24480 oryctolagus
14	40	57.1	148	1 CLM4_MOUSE	Q9jm83 mus musculus
15	40	57.1	198	1 GCAL_CHICK	P79880 gallus galli
16	40	57.1	201	1 GCAL_HUMAN	P43080 homo sapien
17	40	57.1	201	1 GCAL_MOUSE	P43081 mus musculus
18	40	57.1	204	1 GCAL_BOVIN	P46065 bos taurus
19	40	57.1	204	1 GCAL_RABIT	Q9j761 rana pipien
20	40	57.1	273	1 YUBP_ECOLI	P18005 escherichia
21	40	57.1	373	1 GRAC_BACSU	P07870 bacillus su
22	40	57.1	776	1 PSAB_HETTR	Q9xqv2 heterocapsa
23	40	57.1	1217	1 ITN1_RAT	Q9wve9 rattus norv
24	40	57.1	3969	1 HRX_HUMAN	Q03164 homo sapien
25	39	55.7	105	1 S111_HUMAN	P31949 homo sapien
26	39	55.7	143	1 SM16_SCHNA	Q07167 schistosoma
27	39	55.7	245	1 HIS4_YERPE	Q8zfx9 versinia pe
28	39	55.7	251	1 FGFN_MOUSE	Q9epc2 mus musculus
29	39	55.7	276	1 SEGN_HUMAN	O76038 homo sapien
30	39	55.7	334	1 GUB_CLOTM	P29716 clostridium
31	39	55.7	403	1 NOF2_DROME	P15297 drosophila
32	39	55.7	473	1 MPI3_HUMAN	P30307 homo sapien
33	39	55.7	502	1 MPI3_PIG	Q29029 sus scrofa

34	39	55.7	649	1 GUND_CLOTM	P04954 clostridium
35	39	55.7	837	1 PHLD_MOUSE	O70362 mus musculus
36	39	55.7	840	1 PHL1_HUMAN	P80108 homo sapien
37	39	55.7	984	1 NOF_DROME	P16320 drosophila
38	39	55.7	2365	1 CCAH_MOUSE	O88427 mus musculus
39	38	54.3	101	1 S111_CHICK	P24479 gallus galli
40	38	54.3	152	1 SPIA_STRPU	P04109 strongyloce
41	38	54.3	165	1 POC2_JUNOX	O64943 juniperus o
42	38	54.3	244	1 HIS4_MYCLE	Q9cc56 mycobacteri
43	38	54.3	256	1 CSEN_HUMAN	Q9j2w7 homo sapien
44	38	54.3	256	1 CSEN_RAT	Q9j2w7 rattus norv
45	38	54.3	262	1 ENVE_SALTY	Q56032 salmonella

ALIGNMENTS

RESULT 1
RCN1_MOUSE
ID RCN1_MOUSE STANDARD; PRT; 325 AA.
AC Q05186;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Reticulocalbin 1 precursor.
GN RCN1 OR RCN OR RCAL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93107083; PubMed=8416973;
RA Ozawa M., Muramatsu T.;
RT "Reticulocalbin, a novel endoplasmic reticulum resident
Ca(2+)-binding protein with multiple EF-hand motifs and a
carboxyl-terminal HDEL sequence.";
RL J. Biol. Chem. 268:699-705(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SV; TISSUE=Liver;
RC MEDLINE=96015163; PubMed=8537305;
RA Ozawa M.;
RT "Structure of the gene encoding mouse reticulocalbin, a novel
endoplasmic reticulum-resident Ca(2+)-binding protein with multiple
EF-hand motifs.";
RL J. Biochem. 118:154-160(1995).
RN [3]
RP SEQUENCE OF 24-39.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- FUNCTION: MAY REGULATE CALCIUM-DEPENDENT ACTIVITIES IN THE
ENDOPASMIC RETICULUM LUMEN OR POST-ER COMPARTMENT.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
SITES; POTENTIAL SITES II AND VI HAVE LOST AFFINITY FOR CALCIUM.
CC -1- SIMILARITY: BELONGS TO THE CREC FAMILY.
CC -1- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).

EMBL; D13003; BAA02366.1; -;
EMBL; D43956; BAA07896.1; -;

Tue May 20 14:43:33 2003

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EMBL; D43952; BAA07896.1; JOINED.
EMBL; D43954; BAA07896.1; JOINED.
EMBL; D43955; BAA07896.1; JOINED.
PIR; A45337; A45337.
MGD; MGI:104559; Rcn.
InterPro; IPR002048; EF-hand.
InterPro; IPR000886; ER-target.
Pfam; PF00036; ehand; 6.
SMART; SM00054; EFh; 3.
PROSITE; PS00014; ER-TARGET; 1.
PROSITE; PS00018; EF-HAND; 3.
Calcium-binding; Endoplasmic reticulum; Signal; Glycoprotein; Repeat;
Repeat.
SIGNAL 1 23 RETICULOCALBIN 1.
CHAIN 24 325 EF-HAND 1.
CA_BIND 86 97 EF-HAND 2 (POSSIBLY ANCESTRAL).
CA_BIND 122 133 EF-HAND 3.
CA_BIND 173 184 EF-HAND 4.
CA_BIND 210 221 EF-HAND 5.
CA_BIND 251 262 EF-HAND 6 (POSSIBLY ANCESTRAL).
CA_BIND 287 298 PREVENT SECRETION FROM ER.
SITE 322 325 N-LINKED (GLCNAC. .) (PARTIAL).
CARBOHYD 47 47 K -> G (IN REF. 3).
CONFLICT 24 24 R -> I (IN REF. 3).
CONFLICT 34 34 SEL -> DEE (IN REF. 3).
CONFLICT 37 39
SEQUENCE 325 AA; 38113 MW; 0470B10B5A8BC76D CRC64;

Query Match 68.6%; Score 48; DB 1; Length 325;
Best Local Similarity 69.2%; Pred. No. 0.69;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGDLGSGEV 13
Db 251 DLNKGDLKDKDEI 263

RESULT 2
RCN1_HUMAN STANDARD; PRT; 331 AA.
AC Q15293;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Reticulocalbin 1 precursor.
GN RCN1 OR RCN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96172582; PubMed=85866628;
RA Ozawa M.;
RT "Cloning of a human homologue of mouse reticulocalbin reveals
conservation of structural domains in the novel endoplasmic reticulum
resident Ca(2+)-binding protein with multiple EF-hand motifs.";
RL J. Biochem. 117:1113-1119(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Coville G.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY REGULATE CALCIUM-DEPENDENT ACTIVITIES IN THE
ENDOPLASMIC RETICULUM LUMEN OR POST-ER COMPARTMENT.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
SITES; POTENTIAL SITES II AND VI HAVE LOST AFFINITY FOR CALCIUM
(BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CREC FAMILY.
CC -1- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -

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EMBL; D42073; BAA07670.1;
EMBL; AL078612; CAB53067.1;
Genew; HGNC:9934; RCN1.
MIM; 602735;
InterPro; IPR002048; EF-hand.
InterPro; IPR000886; ER-target.
Pfam; PF00036; ehand; 6.
SMART; SM00054; EFh; 3.
PROSITE; PS00014; ER-TARGET; 1.
PROSITE; PS00018; EF-HAND; 4.
Calcium-binding; Endoplasmic reticulum; Signal; Glycoprotein; Repeat;
Polymorphism.
SIGNAL 1 29 RETICULOCALBIN 1.
CHAIN 30 331 EF-HAND 1 (POTENTIAL).
CA_BIND 92 103 EF-HAND 2 (POSSIBLY ANCESTRAL).
CA_BIND 128 139 EF-HAND 3 (POTENTIAL).
CA_BIND 179 190 EF-HAND 4 (POTENTIAL).
CA_BIND 216 227 EF-HAND 5 (POTENTIAL).
CA_BIND 257 268 EF-HAND 6 (POSSIBLY ANCESTRAL).
CA_BIND 293 304 PREVENT SECRETION FROM ER.
SITE 328 331 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 53 53 T -> N (IN DBSNP:1061145).
VARIANT 71 71 /FTID=VAR_011964.
VARIANT 73 73 D -> Y (IN DBSNP:1804281).
VARIANT 74 74 Q -> E (IN DBSNP:1061143).
VARIANT 188 188 /FTID=VAR_011966.
VARIANT 188 188 R -> P (IN DBSNP:1061080).
SEQUENCE 331 AA; 38890 MW; 608AD53693F789 CRC64;

Query Match 68.6%; Score 48; DB 1; Length 331;
Best Local Similarity 69.2%; Pred. No. 0.7;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGDLGSGEV 13
Db 257 DLNKGDLKDKDEI 269

RESULT 3
PPE2_HUMAN STANDARD; PRT; 753 AA.
AC Q14830; O14831;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine/threonine protein phosphatase with EF-hands-2 (BC 3.1.3.16)
DE (PPEF-2).
GN PPEF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS PPEF-2(S) AND PPEF-2(L)).
RC TISSUE=Retina;
RX MEDLINE=97471020; PubMed=9326663;
RA Sherman P.M., Sun H., Macke J.P., Williams J., Smallwood P.M.,
Nathan J.;
RT "Identification and characterization of a conserved family of protein
serine/threonine phosphatases homologous to Drosophila retinal
degeneration C (rdgc).";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11639-11644(1997).
CC -1- FUNCTION: MAY PLAY A ROLE IN PHOTOTRANSDUCTION. MAY
DEPHOSPHORYLATE PHOTOACTIVATED RHODOPSIN. MAY FUNCTION AS A

CC CALCIUM SENSING REGULATOR OF IONIC CURRENTS, ENERGY PRODUCTION OR
 CC SYNAPTIC TRANSMISSION.
 CC -|- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O -> a protein +
 CC phosphate.
 CC -|- COFACTOR: MAGNESIUM (BY SIMILARITY).
 CC -|- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
 CC -|- SUBCELLULAR LOCATION: LOCALIZED TO PHOTORECEPTORS, PPEF-2(L) IS AT
 CC LEAST 2 FOLD MORE ABUNDANT IN ROD INNER SEGMENTS THAN IN THE OUTER
 CC SEGMENTS.
 CC -|- ALTERNATIVE PRODUCTS: 2 ISOFORMS; PPEF-2(L) (SHOWN HERE) AND PPEF-
 CC 2(S); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -|- TISSUE SPECIFICITY: RETINAL SPECIFIC (PROBABLE).
 CC -|- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES.
 CC -|- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES.
 CC -|- SIMILARITY: CONTAINS 1 IQ DOMAIN.
 CC -|- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch)
 CC -----
 CC EMBL; AF023456; AAB82796.1; -
 CC EMBL; AF023457; AAB82797.1; -
 CC HSSP; P08129; 1FJM
 CC Genew; HGNC:9244; PPEF2.
 CC MIM; 602256; -
 CC InterPro; IPR002048; EF-hand.
 CC InterPro; IPR000048; IQ-region.
 CC InterPro; IPR004843; M-ppestrase.
 CC Pfam; PF00036; ehand; 3.
 CC Pfam; PF00149; Metallophos; 1.
 CC Pfam; PF00612; IQ; 1.
 CC PRINTS; PR00114; STPHPTASE.
 CC ProDom; PD000012; EF-hand; 1.
 CC ProDom; PD000252; S/T_phosphatase; 2.
 CC SMART; SM00054; EFh; 2.
 CC SMART; SM00015; IQ; 1.
 CC SMART; SM00156; PP2AC; 1.
 CC PROSITE; PS00018; EF-HAND; 2.
 CC PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
 CC PROSITE; PS00096; IQ; 1.
 CC Hydrolase; Calcium-binding; Magnesium; Iron; Manganese; Repeat;
 CC Vision.
 CC FT DOMAIN 21 46
 CC FT DOMAIN 128 540
 CC FT CA_BIND 665 676
 CC FT CA_BIND 705 716
 CC FT METAL 179 199
 CC FT METAL 181 208
 CC FT METAL 208 220
 CC FT METAL 240 241
 CC FT ACT_SITE 241 241
 CC FT METAL 292 292
 CC FT METAL 488 488
 CC FT VARSPLIC 588 598
 CC FT VARSPLIC 599 753
 CC FT VARIANT 120 120
 CC SEQUENCE 753 AA; 86430 MW; 289DMAC240193A0D CRC64;
 CC /FTId=VAR_010230.
 CC
 CC Query Match 67.18; Score 47; DB 1; Length 753;
 CC Best Local Similarity 66.78; Pred. No. 2.4;
 CC Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC Qy 1 DLNKGDLGSGE 12
 CC I | | | | | : | |
 CC Db 705 DFNKGHDIDINE 716

RESULT 4
 PPE2_MOUSE
 ID PPE2_MOUSE STANDARD; PRT; 757 AA.
 AC O35385;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Serine/threonine protein phosphatase with EF-hands-2 (EC 3.1.3.16)
 DE (PPEF-2).
 GN PPEF2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=97471020; PubMed=9326663;
 RA Sherman P.M., Sun H., Macke J.P., Williams J., Smallwood P.M.,
 RA Nathans J.;
 RT "Identification and characterization of a conserved family of protein
 RT serine/threonine phosphatases homologous to Drosophila retinal
 RT degeneration C (rdgc).";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11639-11644(1997).
 CC -|- FUNCTION: MAY PLAY A ROLE IN PHOTOTRANSDUCTION. MAY
 CC DEPHOSPHORYLATE PHOTOACTIVATED RHODOPSIN. MAY FUNCTION AS A
 CC CALCIUM SENSING REGULATOR OF IONIC CURRENTS, ENERGY PRODUCTION OR
 CC SYNAPTIC TRANSMISSION.
 CC -|- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O -> a protein +
 CC phosphate.
 CC -|- COFACTOR: MAGNESIUM (BY SIMILARITY).
 CC -|- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
 CC -|- TISSUE SPECIFICITY: DETECTED IN RETINA, MORE SPECIFICALLY IN
 CC PHOTORECEPTORS
 CC -|- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES.
 CC -|- SIMILARITY: CONTAINS 1 IQ DOMAIN.
 CC -|- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC -----
 CC EMBL; AF023456; AAB82798.1; -
 CC HSSP; P08129; 1FJM.
 CC MGD; MGI:1342304; Ppef2
 CC InterPro; IPR002048; EF-hand.
 CC InterPro; IPR000048; IQ-region.
 CC InterPro; IPR004843; M-ppestrase.
 CC Pfam; PF00036; ehand; 3.
 CC Pfam; PF00149; Metallophos; 1.
 CC Pfam; PF00612; IQ; 1.
 CC PRINTS; PR00114; STPHPTASE.
 CC ProDom; PD000012; EF-hand; 1.
 CC ProDom; PD000252; S/T_phosphatase; 2.
 CC SMART; SM00054; EFh; 2.
 CC SMART; SM00015; IQ; 1.
 CC SMART; SM00156; PP2AC; 1.
 CC PROSITE; PS00018; EF-HAND; 3.
 CC PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
 CC PROSITE; PS00096; IQ; 1.
 CC Hydrolase; Calcium-binding; Magnesium; Iron; Manganese; Repeat;
 CC Vision.
 CC FT DOMAIN 21 46
 CC FT DOMAIN 128 544
 CC FT CA_BIND 669 680
 CC FT CA_BIND 709 720
 CC CATALYTIC.
 CC ANCESTRAL CALCIUM SITE.
 CC EF-HAND 1 (POTENTIAL).
 CC EF-HAND 2 (POTENTIAL).
 CC IRON (BY SIMILARITY).
 CC IRON (BY SIMILARITY).
 CC IRON AND MANGANESE (BY SIMILARITY).
 CC MANGANESE (BY SIMILARITY).
 CC GENERAL ACID (BY SIMILARITY).
 CC MANGANESE (BY SIMILARITY).
 CC MANGANESE (BY SIMILARITY).
 CC ITLSDWAAAVE -> ASSQLCYQQK (IN ISOFORM
 CC PPEF-2(S)).
 CC MISSING (IN ISOFORM PPEF-2(S)).
 CC S -> R.
 CC /FTId=VAR_010230.

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FT METAL 179 179 IRON (BY SIMILARITY).
FT METAL 181 181 IRON (BY SIMILARITY).
FT METAL 208 208 IRON AND MANGANESE (BY SIMILARITY).
FT METAL 240 240 MANGANESE (BY SIMILARITY).
FT ACT_SITE 241 241 GENERAL ACID (BY SIMILARITY).
FT METAL 292 292 MANGANESE (BY SIMILARITY).
FT METAL 492 492 MANGANESE (BY SIMILARITY).
FT METAL 757 757 AA; 86644 MW; 821B3D1061AC00C8 CRC64;
SQ SEQUENCE 757 AA; 86644 MW; 821B3D1061AC00C8 CRC64;

Query Match. 67.1%; Score 47; DB 1; Length 757;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHDGSEV 12
| | | | | : |
Db 709 DFNKGHDIDNE 720

RESULT 5
NAGH_CLOPE STANDARD; PRT; 1628 AA.
ID NAGH_CLOPE STANDARD; PRT; 1628 AA.
AC P26831;
DT 01-AUG-1992 (Rel. 23, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hyaluronoglucosaminidase precursor (EC 3.2.1.35) (Hyaluronidase)
DE (Mu toxin).
GN NAGH OR CPE0191.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CPN50.
RC MEDLINE=94322189; PubMed=8177218;
RA Canard B., Garnier T., Saint-Joanis B., Cole S.T.;
RA "Molecular genetic analysis of the nagH gene encoding a hyaluronidase
of Clostridium perfringens.";
RT Mol. Gen. Genet. 243:215-224(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=13 / Type A;
RX PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RA "Complete genome sequence of Clostridium perfringens, an anaerobic
flesh-eater.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
RL -1- FUNCTION: Putative virulence factor which is likely to act on
connective tissue during gas gangrene.
CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-linkages between N-
acetyl-beta-D-glucosamine and D-glucuronate residues in
hyaluronate.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- CAUTION: The partially purified protein from strain CPN50 is
approximately 70 kDa smaller than the sequence indicated here.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M61878; AAC23259.1;
CC DR EMBL: AF003185; BAB79897.1;
CC DR PIR: S27540; S27540.
CC DR InterPro: IPR002105; Dockerin_1.
CC DR InterPro: IPR000421; FA58_C.
CC DR Pfam: PF00404; Dockerin_1; 2.
CC DR Pfam: PF00754; F5_F8_type_C; 1.

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DR SMART: SM00231; FA58C; 1.
KW Hydrolase; Glycosidase; Toxin; Repeat; Signal; Complete proteome.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 1628 HYALURONOGUCOSAMINIDASE.
FT DOMAIN 703 1032 3 X APPROXIMATE REPEATS.
FT REPEAT 703 748 1.
FT REPEAT 848 894 2.
FT REPEAT 987 1032 3.
FT VARIANT 147 147 G -> A (IN STRAIN CPN50).
FT VARIANT 172 175 KIQS -> EIKN (IN STRAIN CPN50).
FT VARIANT 250 250 V -> M (IN STRAIN CPN50).
FT VARIANT 548 548 A -> E (IN STRAIN CPN50).
FT VARIANT 558 558 D -> E (IN STRAIN CPN50).
FT VARIANT 614 614 G -> S (IN STRAIN CPN50).
FT VARIANT 944 944 I -> V (IN STRAIN CPN50).
FT VARIANT 950 950 N -> S (IN STRAIN CPN50).
FT VARIANT 979 979 T -> I (IN STRAIN CPN50).
FT VARIANT 982 982 I -> L (IN STRAIN CPN50).
FT VARIANT 1042 1042 I -> F (IN STRAIN CPN50).
FT VARIANT 1043 1042 MISSING (IN STRAIN CPN50).
FT VARIANT 1628 1628 MW; D4252A2512BBED69 CRC64;
SQ SEQUENCE 1628 AA; 182474 MW; D4252A2512BBED69 CRC64;

Query Match. 62.9%; Score 44; DB 1; Length 1628;
Best Local Similarity 61.5%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGHDGSEV 13
| | | | | : |
Db 1607 DLNKGDSIDEYEI 1619

RESULT 6
PPEL_HUMAN STANDARD; PRT; 653 AA.
ID PPEL_HUMAN STANDARD; PRT; 653 AA.
AC O14829; O15253; Q9UJH0; Q9NU21;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine/threonine protein phosphatase with EF-hands-1 (EC 3.1.3.16)
DE (PPEF-1) (Protein phosphatase with EF calcium-binding domain) (PPEF)
DE (Serine/threonine protein phosphatase 7) (PF7).
GN PPEF1 OR PPEF OR PPP7C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=97471020; PubMed=9326663;
RA Sherman P.M., Sun H., Macke J.P., Williams J., Smallwood P.M.,
RA Nathans J.;
RA "Identification and characterization of a conserved family of protein
serine/threonine phosphatases homologous to Drosophila retinal
degeneration C.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:11639-11644(1997).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Fetal brain;
RX MEDLINE=97358589; PubMed=9215685;
RA Montini E., Rugarli E.I., van de Vosse E., Andolfi G., Mariani M.,
RA Puca A.A., Consales G.G., den Dunnen J.F., Ballabio A., Franco B.;
RA "A novel human serine-threonine phosphatase related to the Drosophila
retinal degeneration C (rdgC) gene is selectively expressed in sensory
neurons of neural crest origin.";
RT Hum. Mol. Genet. 6:1137-1145(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=98104127; PubMed=9430683;
RA Huang X., Honkanen R.E.;
RA "Molecular cloning, expression, and characterization of a novel human
serine/threonine protein phosphatase, PP7, that is homologous to

```


RT Drosophila retinal degeneration C gene product (rdgC).";
 RL J. Biol. Chem. 273:1462-1468(1998).
 RN [4]
 RP SEQUENCE OF 1-355 FROM N.A.
 RA Grafham D.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 356-653 FROM N.A.
 RA Wray P.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY HAVE A ROLE IN THE RECOVERY OR ADAPTATION RESPONSE
 CC OF PHOTORECEPTORS. MAY HAVE A ROLE IN DEVELOPMENT. MAXIMAL
 CC ACTIVITY IS OBSERVED AT PH 8.0.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O -> a protein +
 CC phosphate.
 CC -1- COFACTOR: MAGNESIUM.
 CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1 (SHOWN HERE), 1A, 1B, 2 AND 3;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORM 3 MAY HAVE NO
 CC FUNCTIONAL SIGNIFICANCE.
 CC -1- TISSUE SPECIFICITY: DETECTED IN RETINA AND RETINAL DERIVED Y-79
 CC RETINOBLASTOMA CELLS. ALSO FOUND IN FETAL BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES.
 CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF023455; AAB82795.1;
 DR EMBL; X97867; CAA66461.1;
 DR EMBL; AF027977; AAC05825.1;
 DR EMBL; 294056; CAB40074.1;
 DR EMBL; AL096700; CAB86407.1;
 DR HSSP; P08129; IFUM.
 DR Genew; HGNC:9243; PPEFT.
 DR MIM; 300109;
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000048; IQ-region.
 DR InterPro; IPR004843; M-peptase.
 DR InterPro; IPR004844; S/T-phosphatase.
 DR Pfam; PF00036; ehand; 3.
 DR Pfam; PF00149; Metallophos; 1.
 DR PRINTS; PR00114; STPHPTASE.
 DR ProDom; PD000012; EF-hand; 1.
 DR ProDom; PD000252; S/T-phosphatase; 2.
 DR SMART; SM00054; Efh; 2.
 DR SMART; SM00015; IQ; 1.
 DR SMART; SM00156; PF2AC; 1.
 DR PROSITE; PS00018; EF-HAND; 2.
 DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
 DR PROSITE; PS50096; IQ; 1.
 DR KW Hydrolyase; Calcium-binding; Magnesium; Iron; Manganese; Repeat;
 KW Alternative splicing.
 FT DOMAIN 18 43
 FT CATALYTIC. 121 455
 FT ANCESTRAL CALCIUM SITE. 456 507
 FT CA_BIND 579 590
 FT EF-HAND 1 (POTENTIAL). 619 630
 FT EF-HAND 2 (POTENTIAL). 172 172
 FT IRON (BY SIMILARITY). 174 174
 FT IRON (BY SIMILARITY). 201 201
 FT IRON AND MANGANESE (BY SIMILARITY). 233 233
 FT MANGANESE (BY SIMILARITY). 234 234
 FT GENERAL ACID (BY SIMILARITY). 285 285
 FT MANGANESE (BY SIMILARITY). 403 403
 FT MANGANESE (BY SIMILARITY). 79 132
 FT MISSING (IN ISOFORM 1A).
 FT VARSPLIC

FT VARSPLIC 328 355 MISSING (IN ISOFORM 1B).
 FT VARSPLIC 356 376 IIDILSDPRKNGCFPTCR -> SGYYGQRHQIKRES
 FT DFTKK (IN ISOFORM 2).
 FT VARSPLIC 377 653 MISSING (IN ISOFORM 2).
 FT VARSPLIC 356 417 MISSING (IN ISOFORM 3).
 FT CONFLICT 367 367 K -> T (IN REF. 2).
 SQ SEQUENCE 653 AA; 75792 MW; DF7B78C44EE6484 CRC64;
 Query Match 61.4%; Score 43; DB 1; Length 653;
 Best Local Similarity 66.7%; Pred. No. 9.7;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DLNKDGHLDGSE 12
 Db 619 DLNKDGSIDFNE 630
 ||||| : : :
 RESULT 7
 YAE8_YEAST STANDARD; PRT; 662 AA.
 ID YAE8_YEAST
 AC P39722; 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DE 01-OCT-1996 (Rel. 34, Last annotation update)
 GN Hypothetical 75.2 kDa protein in ACS1-GCV3 intergenic region.
 DE YAL048C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC NCB1_TaxID=4912;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=S288C / AB972;
 RX MEDLINE=95249563; Pubmed=7731988;
 RA Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
 RA Hall J., Quellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
 RA Storms R.K.;
 RT "The nucleotide sequence of chromosome I from Saccharomyces
 cerevisiae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
 CC -----
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 CC -----
 DR EMBL; U12980; AAC04983.1;
 DR SGD; S0000046; YAL048C.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR005223; Small_GTP.
 DR InterPro; IPR003575; Small_GTPase.
 DR Pfam; PF00036; ehand; 2.
 DR SMART; SM00010; small_GTPase; 1.
 DR TIGRFAMs; TIGR00231; small_GTP; 2.
 DR KW Hypothetical protein.
 SQ SEQUENCE 662 AA; 75150 MW; A68CDA15D79E5910 CRC64;
 Query Match 61.4%; Score 43; DB 1; Length 662;
 Best Local Similarity 53.8%; Pred. No. 9.9;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DLNKDGHLDGSEV 13
 Db 214 DLNQDSYLDNDNEI 226
 ||||| : : :
 RESULT 8
 ITN2_MOUSE STANDARD; PRT; 1658 AA.
 ID ITN2_MOUSE
 AC Q9Z0R6; Q9Z0R5;

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DR PROSITE: PS50031; EH: 2;
DR PROSITE: PS50003; PH: DOMAIN; 1.
DR PROSITE: PS50002; SH3; 5. Repeat; Coiled coil; Calcium-binding;
KW Endocytosis; SH3 domain;
KW Alternative splicing.
FT DOMAIN 21 109 EH 1.
FT CA_BIND 66 78 EF_HAND (POTENTIAL).
FT DOMAIN 244 333 EH 2.
FT DOMAIN 364 716 COILED COIL (POTENTIAL).
FT DOMAIN 717 778 SH3 1.
FT DOMAIN 851 909 SH3 2.
FT DOMAIN 941 999 SH3 3.
FT DOMAIN 1013 1077 SH3 4.
FT DOMAIN 1087 1146 SH3 5.
FT DOMAIN 1169 1356 DH.
FT DOMAIN 1395 1505 PH.
FT DOMAIN 1517 1613 C2 DOMAIN.
FT VARSPLIC 1187 1197 DDLQLVIEVFQ -> GLQLFEQKTL (IN ISOFORM
2)
FT VARSPLIC 1198 1658 MISSING (IN ISOFORM 2).
FT CONFLICT 451 452 KQ -> NT (IN REF. 1: AAD19748).
FT CONFLICT 1161 1161 D -> G (IN REF. 1: AAD19748).
FT SEQUENCE 1658 AA; 188776 MW; 7050EFC3F7983A5 CRC64;
SQ
Query Match 61.4%; Score 43; DB 1; Length 1658;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DLNKGHLDGSE 12
Db 66 DLNKGDKMDQEE 77

RESULT 9
ITN2_HUMAN STANDARD; PRT: 1696 AA.
ID Q9NZM3; Q9NVG0; Q9ULG4; Q9NZM2; Q9HAK4; Q9NXXE6; Q95062; Q15812;
AC 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Intersectin 2 (SH3 domain-containing protein 1B) (SH3P18) (SH3P18-like
WASP associated protein).
DE ITSN2 OR SH3D1B OR SWAP OR KIAA1256.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RC TISSUE=Fetal brain, and Fetal liver;
RX MEDLINE=20382722; PubMed=10922467;
RA Pucharcos C., Estivill X., de la Luna S.;
RT "Intersectin 2, a new multimodular protein involved in clathrin-
mediated endocytosis."
RL FEBS Lett. 478:43-51(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Seifert M., Engel M., Welter C.;
RT "Intersectin 2 (SH3D1B), human homolog of mouse Eps2 protein."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=20039619; PubMed=10574462;
RA Nagase T., Ishikawa K.-I., Kikuno R., Hirose M., Nomura N.,
RA Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XV.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro."
RL DNA Res. 6:337-345(1999).
RN [4]
RP SEQUENCE OF 258-720 FROM N.A. (ISOFORM 2), AND SEQUENCE OF 1261-1696
FROM N.A.

```


RC TISSUE-Embryo;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.,
RT "NEDO human cDNA sequencing project.",
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 821-1284 FROM N.A. (ISOFORM 1).
RA Wilson L.A., Fields D., Cruz L., Friesen J., Siminovich K.A.,
RT "SH3P18-like wasp associated protein (SWAP): A multiple SH3 domain
RT containing protein that interacts with WASP.",
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 944-1191 FROM N.A. (ISOFORM 4).
RC TISSUE-Bone marrow;
RX MEDLINE-98294438; PubMed-9630982;
RA Sparks A.B., Hoffman N.G., McConnell S.J., Fowlkes D.M., Kay B.K.,
RT "Cloning of ligand targets: systematic isolation of SH3 domain-
RT containing proteins.",
RL Nat. Biotechnol. 14:741-744(1996).
RN [7]
RP ALTERNATIVE SPLICING
RC TISSUE-Fetal liver, and Brain;
RX MEDLINE-21548826; PubMed-11690630;
RA Pucharcos C., Casas C., Nadal M., Estivill X., de la Luna S.,
RT "The human intersectin genes and their spliced variants are
RT differentially expressed.",
RL Blochim. Biophys. Acta 1521:1-11(2001).
CC -1- FUNCTION: Adapter protein that may provide indirect link between
CC the endocytic membrane traffic and the actin assembly machinery.
CC -1- SUBUNIT: Belongs to a complex that may contain multimers of ITSN1,
CC ITSN2 and Eps15, and different partners according to the step in
CC the endocytic process.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: At least 4 isoforms; 1/ITSN2-L (shown here),
CC 2, 3/ITSN2-S1 and 4/ITSN2-S2/SH3P18; are produced by alternative
CC splicing.
CC -1- TISSUE SPECIFICITY: Ubiquitous. Isoform 1 is primarily expressed
CC in adult heart and liver.
CC -1- MISCELLANEOUS: Overexpression results in the inhibition of the
CC transferrin uptake and the blockage of the clathrin-mediated
CC endocytosis.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EF-HAND CALCIUM-BINDING DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 SH3 DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 EH DOMAINS.
CC -----
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CC -----
CC EMBL; AF182198; AAF59903.1; -
CC EMBL; AF182199; AAF59904.1; -
CC EMBL; AF248540; AAF63600.1; ALT_INIT.
CC EMBL; AB033082; BAA66570.1; ALT_INIT.
CC EMBL; AK021545; BAB13841.1; -
CC EMBL; AK000302; BAA91068.1; -
CC EMBL; AF001630; AAD00899.1; -
CC EMBL; U61167; AAC50593.1; -
CC HSP; P29155; 1SEM.
CC Genes: HGNC:6184; ITSN2.
CC MIM: 604464; -
CC InterPro: IPR000008; C2.
CC InterPro: IPR002048; EF-hand.

DR InterPro: IPR000261; EPS15_repeat.
DR InterPro: IPR001849; PH.
DR InterPro: IPR000219; RhoGEF.
DR InterPro: IPR001452; SH3.
DR Pfam: PF00018; SH3; 5.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00621; RhoGEF; 1.
DR PRINTS; PR00499; P67PHOX.
DR PRINTS; PR00452; SH3DOMAIN.
DR SMART; SM00239; C2; 1.
DR SMART; SM00054; EFh; 2.
DR SMART; SM00027; EH; 2.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00326; SH3; 5.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00010; DH_2; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00031; EH; 2.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00002; SH3; 5.
KW Endocytosis; SH3 domain; Repeat; Coiled coil; Calcium-binding;
KW Alternative splicing.
FT DOMAIN 21 109 EH 1.
FT CA_BIND 66 78 EF-HAND (POTENTIAL).
FT DOMAIN 243 332 EH 2.
FT DOMAIN 360 755 COILED COIL (POTENTIAL).
FT DOMAIN 756 817 SH3 1.
FT DOMAIN 897 955 SH3 2.
FT DOMAIN 980 1038 SH3 3.
FT DOMAIN 1052 1116 SH3 4.
FT DOMAIN 1126 1185 SH3 5.
FT DOMAIN 1208 1394 DH.
FT DOMAIN 1433 1543 PH.
FT DOMAIN 1555 1651 C2 DOMAIN.
FT VARSPLIC 621 647 MISSING (IN ISOFORM 2).
FT VARSPLIC 1234 1248 FQKMAESGFLTEGE -> WRLLASSRGICCLS (IN
FT VARSPLIC 1249 1696 ISOFORM 3).
FT VARSPLIC 1192 1696 MISSING (IN ISOFORM 3).
FT CONFLICT 290 290 MISSING (IN ISOFORM 4).
FT CONFLICT 678 678 V -> I (IN REF. 4).
FT CONFLICT 822 827 KAVSPK -> FFAAST (IN REF. 5).
FT CONFLICT 944 950 WFKSVK -> EFAAST (IN REF. 6).
FT CONFLICT 1278 1284 GKMPVQ -> VDAANS (IN REF. 5).
FT CONFLICT 1552 1552 K -> Q (IN REF. 2 AND 3).
SQ SEQUENCE 1696 AA; 193329 MW; 17B5C8629BCCFF9B CRC64;
Query Match 61.4%; Score 43; DB 1; Length 1696;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DLNKGHLGDS 12
Db 66 DLNKGCKMDQDE 77
RESULT 10
HIS4_PASMU
ID HIS4_PASMU STANDARD; PRT; 249 AA.
AC Q9CLM1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 1-(5-phosphoribosyl)-5-[5-phosphoribosylamino)methylidenamino]
DE imidazole-4-carboxamide isomerase (EC 5.3.1.16)
DE (Phosphoribosylformimino-5-aminimidazole carboxamide ribotide
DE isomerase).
DE HIS4 OR PM1203.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.

Tue May 20 14:43:33 2003

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CC EMBL; J05227; AAA30129.1; -
CC DR PIR; A35535; A35535. DR
CC InterPro; IPR002048; EF-hand. DR
CC Pfam; PF00036; ehand; 4. DR
CC ProDom; PD000012; EF-hand; 2. DR
CC SMART; SM00054; EFh; 4. DR
CC PROSITE; PS00018; EF-hand; 4. DR
CC KQ CALCIUM-BINDING; Repeat. 25 KDA CALCIUM-BINDING PROTEIN.
CC FT CHAIN 1 207 12 KDA CALCIUM-BINDING PROTEIN.
CC FT CHAIN 1 103 BLOCKED.
CC FT MOD_RES 1 1 EF-HAND 1 (POTENTIAL).
CC FT CA_BIND 30 41 EF-HAND 2 (POTENTIAL).
CC FT CA_BIND 73 84 EF-HAND 3 (POTENTIAL).
CC FT CA_BIND 132 143 EF-HAND 4 (POTENTIAL).
CC FT CA_BIND 174 185 EF-HAND 4 (POTENTIAL).
CC SQ SEQUENCE 207 AA; 1932840D4632D571 CRC64;
Query Match 58.6%; Score 41; DB 1; Length 207;
Best Local Similarity 69.2%; Pred. No. 6.6;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DLNKGDLGSEV 13
DB 30 DSNKNGTLDPSEV 42
RESULT 12
CMC3_CAEEL STANDARD; PRT; 587 AA.
ID CMC3_CAEEL AC Q19529;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable calcium-binding mitochondrial carrier Fl7E5.2.
GN Fl7E5.2
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA McMurray A.A.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: CALCIUM-DEPENDENT MITOCHONDRIAL SOLUTE CARRIER (BY
CC -!- SIMILARITY). LOCATION: Integral membrane protein. Mitochondrial
CC -!- SUBCELLULAR LOCATION: Inner membrane (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. ARALAR
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
-----
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-----
CC EMBL; Z50873; CAA90761.2; -
CC WormPep; F17E5.2; CE23667. DR
CC InterPro; IPR002048; EF-hand. DR
CC InterPro; IPR002067; Mit_carrier. DR
CC InterPro; IPR001993; Mitoch_carrier. DR
CC Pfam; PF00036; ehand; 3. DR
CC Pfam; PF00153; mito_carr; 3. DR
CC PRINTS; PR00026; MITOCARRIER. DR
CC ProDom; PD000012; EF-hand; 1. DR
CC SMART; SM00054; EFh; 2. DR
CC PROSITE; PS00018; EF_HAND; 2. DR

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DR PROSITE; PS00215; MITOCH_CARRIER; FALSE_NEG.
 KW Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
 KW Transmembrane; Transport; Calcium-binding;
 FT TRANSMEM 265 282
 FT TRANSMEM 337 356
 FT TRANSMEM 382 395
 FT TRANSMEM 433 452
 FT TRANSMEM 475 492
 FT TRANSMEM 534 551
 FT CA_BIND 49 60
 FT CA_BIND 83 94
 FT DOMAIN 119 129
 FT CA_BIND 149 160
 FT DOMAIN 185 195
 FT REPEAT 185 365
 FT REPEAT 366 459
 FT REPEAT 460 563
 SQ SEQUENCE 587 AA; 65906 MW; 19E62936D5A17021 CRC64;

Query Match 58.6%; Score 41; DB 1; Length 587;
 Best Local Similarity 53.8%; Pred. No. 19;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGCHLDGSEV 13
 ||| ||| :| :|
 Db 149 DLNSDGEVDMAEI 161

RESULT 13
 ID S111_RABIT STANDARD; PRT; 102 AA.
 AC P24480;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calgizarin (S100C protein).
 GN S100A11 OR S100C OR PCALG.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=92095968; PubMed=1836726;
 RA Watanabe M., Ando Y., Todoroki H., Minami H., Hirooyoshi H.;
 RT "Molecular cloning and sequencing of a cDNA clone encoding a new
 RT calcium binding protein, named calgizarin, from rabbit lung.";
 RL Biochem. Biophys. Res. Commun. 181:644-649(1991).
 RN [2]
 RP SEQUENCE OF 35-49 AND 53-62.
 RC TISSUE=Lung;
 RX MEDLINE=92011625; PubMed=1917990;
 RA Todoroki H., Kobayashi R., Watanabe M., Minami H., Hidaka H.;
 RT "Purification, characterization, and partial sequence analysis of a
 RT newly identified EF-hand type 13-kDa Ca(2+)-binding protein from
 RT smooth muscle and non-muscle tissues.";
 RL J. Biol. Chem. 266:18668-18673(1991).
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- MISCELLANEOUS: BINDS TWO CALCIUM IONS PER MOLECULE WITH AN
 CC AFFINITY SIMILAR TO THAT OF THE S-100 PROTEINS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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DR EMBL; D10586; BAA01443.1; -.
 DR PIR; B41004; B41004.
 DR PIR; JQ1300; JQ1300.
 DR HSSP; P31950; IOLS.
 DR InterPro; IPR001751; CAPP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR ProDom; PD000012; EF-hand; 1.
 DR ProDom; PD003407; CAPP_S100; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00303; S100_CAPP; 1.
 FT CA_BIND 22 35
 FT CA_BIND 65 76
 FT CONFLICT 59 59
 FT CONFLICT 59 59
 SQ SEQUENCE 102 AA; 11429 MW; 66D1FFBBA4F8DF45 CRC64;

Query Match 57.1%; Score 40; DB 1; Length 102;
 Best Local Similarity 66.7%; Pred. No. 4.8;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLNKGCHLDGSE 12
 ||| ||| |
 Db 65 DLNSDGLDFQE 76

RESULT 14
 ID CLM4_MOUSE STANDARD; PRT; 148 AA.
 AC Q9JNB3; Q9CR31; Q9DIE9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calmodulin 4 (Calcium-binding protein Dd112).
 GN CALM4 OR DD112.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ikegawa S., Nakamura Y.;
 RT "DD112, a novel mouse gene implicated in the early stage of ectopic
 RT ossification.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stauffer F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boirelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyushaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: IMPLICATED IN THE EARLY STAGE OF ECTOPIC OSSIFICATION.
 CC -1- SIMILARITY: CONTAINS 3 EF-HAND CALCIUM-BINDING DOMAINS.

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 CC EMBL; AB036744; BAA95412.1; -
 CC EMBL; AK009556; BAB26608.1; -
 CC EMBL; AK009664; BAB26425.1; -
 CC EMBL; AK003648; BAB22914.1; -
 CC HSSP; P02593; 1CDM.
 CC MGD; MGI:1931464; Calm4.
 CC InterPro: IPR002048; EF-hand.
 CC InterPro: IPR001125; Recoverin.
 CC Pfam; PF00036; efhand; 4.
 CC PRINTS; PR00450; RECOVERIN.
 CC PRODOM; PD000012; EF-hand; 2.
 CC SMART; SM00054; EFh; 3.
 CC PROSITE; PS00018; EF_HAND; 3.
 CC Calcium-binding; Repeat.
 CC CA_BIND 21 32 EF-HAND 1 (POTENTIAL).
 CC CA_BIND 57 68 EF-HAND 2 (POTENTIAL).
 CC CA_BIND 93 104 EF-HAND 3 (POTENTIAL).
 CC CONFLICT 9 9 E -> V (IN REF. 2; BAB22914).
 CC CONFLICT 124 124 M -> V (IN REF. 2; BAB22914).
 CC CONFLICT 146 148 VEN -> I (IN REF. 1).
 CC SEQUENCE 148 AA; 16767 MW; 2AE22BC738AD2F9D CRC64;
 CC
 CC Query Match 57.1%; Score 40; DB 1; Length 148;
 CC Best Local Similarity 53.8%; Pred. No. 7;
 CC Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC QY 1 DLNKGHLDGSRV 13
 CC DB 21 DLNKGHLDGSRV 33
 CC
 CC RESULT 15
 CC GCAL CHICK STANDARD; PRT; 198 AA.
 CC AC P79880.
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Guanylyl cyclase activating protein 1 (GCAP 1) (Guanylate cyclase
 CC activator 1A).
 CC GUCALIA OR GCAP1.
 CC Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC TISSUE=Retina;
 CC MEDLINE=96200167; PubMed=8641465;
 CC Sample-Rowland S.L.; Gorczyca W.A.; Buczylo J., Helekar B.S.,
 CC Ruiz C.C., Subbaraya I., Palczewski K., Baehr W.;
 CC "Expression of GCAP1 and GCAP2 in the retinal degeneration (rd)
 CC mutant chicken retina."
 CC FEBS Lett. 385:47-52(1996).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=White leghorn; TISSUE=Liver;
 CC MEDLINE=99357925; PubMed=10427104;
 CC Sample-Rowland S.L.; Larkin P., Bronson J.D., Nykamp K., Streit W.J.,
 CC Baehr W.;
 CC "Characterization of the chicken GCAP gene array and analyses of
 CC GCAP1, GCAP2, and GC1 gene expression in normal and rd chicken
 CC pineal."
 CC Mol. Vision 5:14-14(1999).
 CC

CC -!- FUNCTION: STIMULATES GUANYLYL CYCLASE 1 (GC1) WHEN FREE CALCIUM
 CC IONS CONCENTRATION IS LOW AND INHIBITS GC1 WHEN FREE CALCIUM IONS
 CC CONCENTRATION IS ELEVATED. THIS CA(2+)-SENSITIVE REGULATION OF GC
 CC IS A KEY EVENT IN RECOVERY OF THE DARK STATE OF ROD PHOTORECEPTORS
 CC FOLLOWING LIGHT EXPOSURE (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: RETINA, IN ROD AND CONE OUTER SEGMENTS, AND
 CC PINAL GLAND.
 CC -!- MISCELLANEOUS: BINDS THREE CALCIUM IONS (BY SIMILARITY).
 CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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CC -----
 CC EMBL; S82199; AAB47111.1; -
 CC EMBL; AF172707; AAD47879.1; -
 CC HSSP; P51177; 1JBA.
 CC InterPro: IPR002048; EF-hand.
 CC InterPro: IPR001125; Recoverin.
 CC Pfam; PF00036; efhand; 3.
 CC PRINTS; PR00450; RECOVERIN.
 CC PRODOM; PD000012; EF-hand; 1.
 CC SMART; SM00054; EFh; 3.
 CC PROSITE; PS00018; EF_HAND; 3.
 CC Calcium-binding; Repeat; Vision; Myristate.
 CC INIT_MET 0 0 POTENTIAL.
 CC LIPID 1 1 MYRISTATE (POTENTIAL).
 CC DOMAIN 25 36 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
 CC CA_BIND 62 73 EF-HAND 2 (POTENTIAL).
 CC CA_BIND 98 109 EF-HAND 3 (POTENTIAL).
 CC CA_BIND 141 152 EF-HAND 4 (POTENTIAL).
 CC SEQUENCE 198 AA; 22677 MW; 97B876BBFD2EF959 CRC64;
 CC
 CC Query Match 57.1%; Score 40; DB 1; Length 198;
 CC Best Local Similarity 58.3%; Pred. No. 9.3;
 CC Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 CC
 CC QY 1 DLNKGHLDGSE 12
 CC DB 62 DENKDGVIDFME 73
 CC
 CC Search completed: May 14, 2003, 10:43:35
 CC Job time : 3.10557 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:40:47 ; Search time 2.02053 Seconds
(without alignments)
618.525 Million cell updates/sec

Title: US-09-768-840-1-copy_254_266
Perfect score: 70
Sequence: 1 DLNKGDLGSEV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	68.6	325	2 A45337	reticulocalbin pre
2	48	68.6	331	2 JC4173	reticulocalbin pre
3	46	65.7	170	2 T24463	hypothetical prote
4	45	64.3	289	2 E81259	hypothetical prote
5	43	61.4	163	2 JMO062	fast skeletal trop
6	43	61.4	163	2 JMO063	fast skeletal trop
7	43	61.4	236	2 T33406	hypothetical prote
8	43	61.4	562	2 S51971	probable membrane
9	43	61.4	1181	2 C86349	F8K7.4 protein - A
10	42	60.0	142	2 T02387	hypothetical prote
11	42	60.0	186	2 T22685	hypothetical prote
12	42	60.0	574	2 G96572	hypothetical prote
13	42	60.0	1636	2 B82736	protein F12M16.12
14	41	58.6	207	2 A35535	hemolysin-type cal
15	41	58.6	282	2 H81358	23K calcium-bindin
16	41	58.6	322	2 A57516	probable signal pe
17	41	58.6	374	2 A42264	DNA supercoiling f
18	41	58.6	475	2 T50686	membrane-associate
19	41	58.6	531	2 G89667	peroxisomal Ca-dep
20	41	58.6	587	2 T21074	protein F17E5.2 (i
21	41	58.6	3110	2 AC0116	hypothetical prote
22	40	57.1	102	1 JQ1300	probable virulence
23	40	57.1	133	2 S68589	calgizarrin - rabb
24	40	57.1	199	2 S68338	EF hand domain pro
25	40	57.1	201	2 C55331	guanylate cyclase
26	40	57.1	202	2 B53311	guanylate cyclase
27	40	57.1	273	2 S07014	guanylate cyclase
28	40	57.1	273	2 JN0037	hypothetical prote
29	40	57.1	313	2 T33849	hypothetical prote

30 40 57.1 373 2 G69629 germination respon

31 40 57.1 373 2 B26470 spore germination

32 40 57.1 530 2 A84847 probable Ca2+ depe

33 40 57.1 751 2 T34490 hypothetical prote

34 40 57.1 3968 2 A44265 trichorax homolog

35 39 55.7 97 2 F82722 hypothetical prote

36 39 55.7 105 1 I37080 calgizarrin - huma

37 39 55.7 178 2 G96667 calgizarrin - huma

38 39 55.7 237 2 T26660 unknown protein, 5

39 39 55.7 245 2 AD0188 hypothetical prote

40 39 55.7 251 2 JC7513 1-(5-phosphoribosy

41 39 55.7 334 1 S23498 fibroblast growth

42 39 55.7 342 2 E89876 licheninase (EC 3.

43 39 55.7 403 2 S07825 hypothetical prote

44 39 55.7 436 2 A83909 hypothetical prote

45 39 55.7 473 1 A38874 protein-tyrosine-p

ALIGNMENTS

RESULT 1
A45337
reticulocalbin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002
C:Accession: A45337; I55203
R:Ozawa, M.; Muramatsu, T.
J. Biol. Chem. 268, 699-705, 1993
A:Title: Reticulocalbin, a novel endoplasmic reticulum resident Ca(2+)-binding prote
A:Reference number: A45337; MUID:9107083; PMID:8416973
A:Contents: teratocarcinoma OTT6050
A:Accession: A45337
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-325 <OJA>
A:Cross-references: GB:D13003; NID:g220581; PIDN:BAA02366.1; PID:d1002865; PID:g22058
A:Note: sequence extracted from NCBI backbone (NCBIP:121512)
R:Ozawa, M.
J. Biochem. 118, 154-160, 1995
A:Title: Structure of the gene encoding mouse reticulocalbin, a novel endoplasmic re.
A:Reference number: I55203; MUID:96015163; PMID:8537305
A:Accession: I55203
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-325 <RES>
A:Cross-references: GB:D43956; NID:g2150295; PIDN:BAA07896.1; PID:g968894
C:Genetics:
A:Introns: 79/2; 144/1; 203/3; 224/1; 290/3
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: EF hand
F:1-23/Domain: signal sequence #status predicted <SIG>
F:322-325/Region: endoplasmic reticulum retention signal

Query Match 68.6%; Score 48; DB 2; Length 325;
Best Local Similarity 69.2%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DLNKGDLGSEV 13

DB 251 DLNKGDLKDEI 263

RESULT 2

JC4173
reticulocalbin precursor - human
C:Species: Homo sapiens (man)
C:Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 02-Aug-2002
C:Accession: JC4173
R:Ozawa, M.
J. Biochem. 117, 1113-1119, 1995
A:Title: Cloning of a human homologue of mouse reticulocalbin reveals conservation of

us-09-768-840-1_copy_254_266.rpr

Tue May 20 14:43:32 2003

```

A:Reference number: JCA173; MUID:96172582; PMID:8586628
A:Accession: JCA173
A:Molecule type: DNA
A:Residues: 1-289 <PAR>
A:Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73619.1; PID:g9696
A:Experimental source: serotype O2, strain NCTC 11168
C:Comment: This protein is a luminal protein of the endoplasmic reticulum, and is a Ca2+
a signal for its retention in the endoplasmic reticulum of cells.
C:Genetics:
A:Gene: GDB:RCN; Rcal
A:Cross-references: GDB:6383031
A:Map position: lrp3-llp3
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: calcium binding; calmodulin binding; EF hand; endoplasmic reticulum
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-331/Product: reticulocalbin homolog #status predicted <MAT>
F:79-111/Domain: calmodulin repeat homology <EF1>
F:113-145/Domain: calmodulin repeat homology <EF2>
F:166-198/Domain: calmodulin repeat homology <EF3>
F:203-235/Domain: calmodulin repeat homology <EF4>
F:244-276/Domain: calmodulin repeat homology <EF5>
F:280-312/Domain: calmodulin repeat homology <EF6>
F:328-331/Region: endoplasmic reticulum retention signal

Query Match 68.6%; Score 48; DB 2; Length 331;
Best Local Similarity 69.2%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 3;

QY 1 DLNKGHLGDSGV 13
||||| |||
Db 257 DLNKGKLDKDEI 269

RESULT 3
T24463
hypothetical protein T04F3.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24463
R:Kershaw, J.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19894
A:Accession: T24463
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-170 <WIL>
A:Cross-references: EMBL:Z72513; PIDN:CAA96671.1; GSPDB:GN00023; CESP:T04F3.4
A:Experimental source: clone T04F3
C:Genetics:
A:Gene: CESP:T04F3.4
A:Map position: 5
A:Introns: 65/3; 76/2; 129/1

Query Match 65.7%; Score 46; DB 2; Length 170;
Best Local Similarity 61.5%; Pred. No. 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 3;

QY 1 DLNKGHLGDSGV 13
||||| |||
Db 105 DLNKNFIDGIEI 117

RESULT 4
E81259
hypothetical protein Cj163lc [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C:Accession: E81259
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: E81259

```

```

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <PAR>
A:Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73619.1; PID:g9696
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj163lc

Query Match 64.3%; Score 45; DB 2; Length 289;
Best Local Similarity 61.5%; Pred. No. 5.2; Indels 0; Gaps 0;
Matches 8; Conservative 3; Mismatches 2;

QY 1 DLNKGHLGDSGV 13
||||| |||
Db 165 DVNKGKRVDSGV 177

RESULT 5
JW0062
fast skeletal troponin C alpha - African clawed frog
N:Alternate names: ftnC
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 20-Jun-2000
C:Accession: JW0062
R:Yuasa, H.J.; Cox, J.A.; Takagi, T.
J. Biochem. 123, 1180-1190, 1998
A:Title: Diversity of the troponin C genes during chordate evolution.
A:Reference number: JW0060; MUID:98269050; PMID:9604009
A:Accession: JW0062
A:Molecule type: mRNA
A:Residues: 1-163 <YUA>
A:Cross-references: DBJ:AB003078; NID:g1945532; PIDN:BAA19734.1; PID:g1945533
C:Comment: This protein belongs to the EF-hand Ca2+ binding protein family and functi-
C:Genetics:
A:Introns: 3/3 108/2
A:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand
F:18-50/Domain: calmodulin repeat homology <EF1>
F:54-86/Domain: calmodulin repeat homology <EF2>
F:94-126/Domain: calmodulin repeat homology <EF3>
F:130-162/Domain: calmodulin repeat homology <EF4>

Query Match 61.4%; Score 43; DB 2; Length 163;
Best Local Similarity 53.8%; Pred. No. 6.2; Indels 0; Gaps 0;
Matches 7; Conservative 3; Mismatches 3;

QY 1 DLNKGHLGDSGV 13
||||| |||
Db 107 DKNADGYIDGEEL 119

RESULT 6
JW0063
fast skeletal troponin C beta - African clawed frog
N:Alternate names: ftnC
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 20-Jun-2000
C:Accession: JW0063
R:Yuasa, H.J.; Cox, J.A.; Takagi, T.
J. Biochem. 123, 1180-1190, 1998
A:Title: Diversity of the troponin C genes during chordate evolution.
A:Reference number: JW0060; MUID:98269050; PMID:9604009
A:Accession: JW0063
A:Molecule type: mRNA
A:Residues: 1-163 <YUA>
A:Cross-references: DBJ:AB003079; NID:g1945534; PIDN:BAA19735.1; PID:g1945535
C:Comment: This protein belongs to the EF-hand Ca2+ binding protein family and functi-
C:Genetics:
A:Introns: 3/3 108/2
A:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand
F:18-50/Domain: calmodulin repeat homology <EF1>
F:54-86/Domain: calmodulin repeat homology <EF2>

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F:94-126/Domain: calmodulin repeat homology <EF3>
F:130-162/Domain: calmodulin repeat homology <EF4>

Query Match 61.4%; Score 43; DB 2; Length 163;
Best Local Similarity 53.8%; Pred. No. 6.2;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGCHLDGSEV 13
| | | | | | | | | |
Db 107 DKNADGYIDGEEL 119

RESULT 7
T33406
hypothetical protein H10E21.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T33406

R:Davidson, S.; Wohldmann, P.; Courtney, L.
submitted to the EMBL Data Library, July 1998
A:Description: The sequence of C. elegans cosmid H10E21.
A:Reference number: 221339

A:Accession: T33406
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-236 <DAV>

A:Cross-references: EMBL:AF078783; PIDN:AC26922.1; GSPDB:GN00021; CESP:H10E21.4
A:Experimental source: strain Bristol N2; clone H10E21
C:Genetics:

A:Gene: CESP:H10E21.4
A:Map position: 3
A:Introns: 21/1; 53/1; 116/2; 190/3

Query Match 61.4%; Score 43; DB 2; Length 236;
Best Local Similarity 66.7%; Pred. No. 9.2;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLNKGCHLDGSE 12
| | | | | | | | | |
Db 59 DLDRNGHLDISE 70

RESULT 8
S51971

Probable membrane protein YAL048c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002

C:Accession: S51971
R:Bussey, H.; Kaback, D.B.; Zhong, W.; Vo, D.T.; Clark, M.W.; Fortin, N.; Hall, J.; Ouel

submitted to the EMBL Data Library, August 1994
A:Description: The sequence of chromosome 1 of Saccharomyces cerevisiae.
A:Reference number: S51956

A:Accession: S51971
A:Molecule type: DNA
A:Residues: 1-662 <BUS>

A:Cross-references: EMBL:U12980; NID:gl326053; PID:g595536; GSPDB:GN00001; MIPS:YAL048c
A:Gene: MIPS:YAL048c

A:Cross-references: SGD:S0000046
A:Map position: 1L
C:Keywords: transmembrane protein
F:635-651/Domain: transmembrane #status predicted <TM1>

Query Match 61.4%; Score 43; DB 2; Length 662;
Best Local Similarity 53.8%; Pred. No. 27;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGCHLDGSEV 13
| | | | | | | | | |
Db 214 DLNQDSYLDNEI 226

RESULT 9

C86349

F8K7.4 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alca

ansen, N.F.; Hughes, B.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

Rizzo, M.; Rooney, T.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Matti, R.; Marz

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: C86349

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1181 <STO>

A:Cross-references: GB:AE005172; NID:g5263313; PIDN:AAD41415.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 61.4%; Score 43; DB 2; Length 1181;
Best Local Similarity 58.3%; Pred. No. 48;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGCHLDGSE 12
| | | | | | | | | |
Db 21 DLQGDGHISGAE 32

RESULT 10

T02387

hypothetical protein At2g44310 [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein F4I1.12

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 02-Feb-2001

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.;

submitted to the EMBL Data Library, May 1998

A:Description: Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence.

A:Reference number: Z14667

A:Accession: T02387

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-142 <ROU>

A:Cross-references: EMBL:AC004521; NID:g3128166; PID:g3128177

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

euss, D.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84877

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-142 <STO>

A:Cross-references: GB:AE002093; NID:g3128177; PIDN:AAC16081.1; GSPDB:GN00139

C:Genetics:

A:Gene: AT2g44310; F4I1.12

A:Map position: 2

Query Match 60.0%; Score 42; DB 2; Length 142;
Best Local Similarity 69.2%; Pred. No. 8;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGCHLDGSEV 13
| | | | | | | | | |
Db 33 DLNKGVLRSSEL 45

Tue May 20 14:43:32 2003

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: B82736

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1036 <STM>

A:Cross-references: GB:AE003938; GB:AE003849; NID:9105935; PIDN:AAF83821.1; GSPDB:GN

A:Experimental source: strain 9a5C

R:Simons, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

Submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, R.C.; Miyaki, C.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; palmieri,

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1011

Query Match 60.0%; Score 42; DB 2; Length 1636;

Best Local Similarity 53.8%; Pred. No. 1e+02;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGHLGDSV 13

Db 558 DLNKGHLGDSV 570

RESULT 14

A35535

C:Species: Tetrahymena thermophila

C:Date: 31-Aug-1990 #sequence_revision 18-Nov-1992 #text_change 07-Dec-1999

C:Accession: A35535

R:Takemasa, T.; Takagi, T.; Kobayashi, T.; Konishi, K.; Watanabe, Y.

J. Biol. Chem. 265, 2514-2517, 1990

A:Title: The third calmodulin family protein in Tetrahymena. Cloning of the cDNA for

A:Reference number: A35535; MUID:90153866; PMID:2303413

A:Accession: A35535

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-207 <TAK>

A:Cross-references: GB:J05227; NID:9161860; PID:9161861

A:Note: the authors translated the codon CAA for residue 104 as Glu

C:Genetics:

C:Superfamily: unassigned calmodulin-related proteins; calmodulin repeat homology

C:Keywords: calcium binding; EF hand

Query Match 58.6%; Score 41; DB 2; Length 207;

Best Local Similarity 69.2%; Pred. NO. 17;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGHLGDSV 13

Db 30 DSNKNGTLDPEV 42

RESULT 15

H81358

C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002

C:Accession: H81358

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Ch

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; B

RESULT 11

T22685

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T22685

R:Kershaw, J.

Submitted to the EMBL Data Library, May 1996

A:Reference number: Z19600

A:Accession: T22685

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-186 <WIL>

A:Cross-references: EMBL:Z72511; PIDN:CAA96655.1; GSPDB:GN000023; CESP:F55A11.1

A:Experimental source: clone F55A11

C:Genetics:

A:Gene: CESP:F55A11.1

A:Map position: 5

A:Introns: 33/3; 59/2; 146/2

Query Match 60.0%; Score 42; DB 2; Length 186;

Best Local Similarity 61.5%; Pred. No. 11;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLGDSV 13

Db 89 DLNKGHLGDSV 101

RESULT 12

G96572

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: G96572

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.B.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: G96572

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-574 <STO>

A:Cross-references: GB:AE005173; NID:97769854; PIDN:AAF69532.1; GSPDB:GN00141

C:Genetics:

A:Gene: F12M16.12

A:Map position: 1

Query Match 60.0%; Score 42; DB 2; Length 574;

Best Local Similarity 53.8%; Pred. NO. 34;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLNKGHLGDSV 13

Db 301 DANNDGHLAAEL 313

RESULT 13

B82736

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: B82736

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: H81358
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-282 <PAR>
A:Cross-references: GB:AL139076; GB:AL111168; NID:96968128; PIDN:CAB73121.1; PID:9696830
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: lepP; Cj0856
C:Superfamily: signal peptidase I
C:Keywords: hydrolase; serine proteinase

Query Match 58.6%; Score 41; DB 2; Length 282;
Best Local Similarity 87.5%; Pred. NO. 24;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DLNRDGH 8
Db 73 DENKDGHL 80

Search completed: May 14, 2003, 10:46:31
Job time : 5.02053 secs

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GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 12:18:31 ; Search time 194 Seconds
(without alignments)
2180.926 Million cell updates/sec

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Perfect score: 1772
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Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 810007 seqs, 644969091 residues

Total number of hits satisfying chosen parameters: 1620014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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-NCPU=6 -ICPU=3 -NO_XLPV=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1772	100.0	1463	10	US-09-847-809A-2	Sequence 2, Appl1
3	1772	100.0	1503	9	US-09-905-291A-220	Sequence 220, App
4	1772	100.0	1503	9	US-09-902-853-220	Sequence 220, App

5	1772	100.0	1503	9	US-09-907-824-220	Sequence 220, App
6	1772	100.0	1503	9	US-09-907-841-220	Sequence 220, App
7	1772	100.0	1503	9	US-09-904-011-220	Sequence 220, App
8	1772	100.0	1503	9	US-10-028-072-363	Sequence 363, App
9	1772	100.0	1503	9	US-09-906-742-220	Sequence 220, App
10	1772	100.0	1503	9	US-10-121-049-363	Sequence 363, App
11	1772	100.0	1503	9	US-10-123-904-363	Sequence 363, App
12	1772	100.0	1503	9	US-10-140-470-363	Sequence 363, App
13	1772	100.0	1503	9	US-09-906-838-220	Sequence 220, App
14	1772	100.0	1503	9	US-09-907-942-220	Sequence 220, App
15	1772	100.0	1503	9	US-10-175-746-363	Sequence 363, App
16	1772	100.0	1503	9	US-10-176-918-363	Sequence 363, App
17	1772	100.0	1503	9	US-10-176-921-363	Sequence 363, App
18	1772	100.0	1503	9	US-10-137-865-363	Sequence 363, App
19	1772	100.0	1503	9	US-10-140-474-363	Sequence 363, App
20	1772	100.0	1503	9	US-09-904-820-220	Sequence 220, App
21	1772	100.0	1503	9	US-09-904-859-220	Sequence 220, App
22	1772	100.0	1503	9	US-10-142-431-363	Sequence 363, App
23	1772	100.0	1503	9	US-09-906-646-220	Sequence 220, App
24	1772	100.0	1503	9	US-09-906-700-220	Sequence 220, App
25	1772	100.0	1503	9	US-09-902-903-220	Sequence 220, App
26	1772	100.0	1503	9	US-09-903-749A-220	Sequence 220, App
27	1772	100.0	1503	9	US-09-903-786-220	Sequence 220, App
28	1772	100.0	1503	9	US-09-902-736-220	Sequence 220, App
29	1772	100.0	1503	9	US-09-904-119-220	Sequence 220, App
30	1772	100.0	1503	9	US-09-904-956-220	Sequence 220, App
31	1772	100.0	1503	9	US-10-123-262-363	Sequence 363, App
32	1772	100.0	1503	9	US-10-142-423-363	Sequence 363, App
33	1772	100.0	1503	9	US-09-902-692-220	Sequence 220, App
34	1772	100.0	1503	9	US-09-903-520-220	Sequence 220, App
35	1772	100.0	1503	9	US-09-903-943-220	Sequence 220, App
36	1772	100.0	1503	9	US-09-905-056-220	Sequence 220, App
37	1772	100.0	1503	9	US-09-907-923-220	Sequence 220, App
38	1772	100.0	1503	9	US-09-907-794-220	Sequence 220, App
39	1772	100.0	1503	9	US-10-142-423-363	Sequence 363, App
40	1772	100.0	1503	9	US-09-902-692-220	Sequence 220, App
41	1772	100.0	1503	9	US-09-903-520-220	Sequence 220, App
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43	1772	100.0	1503	9	US-09-905-056-220	Sequence 220, App
44	1772	100.0	1503	9	US-09-907-923-220	Sequence 220, App
45	1772	100.0	1503	9	US-09-907-923-220	Sequence 220, App

ALIGNMENTS

RESULT 1
US-09-768-840-2
; Sequence 2, Application US/09768840
; Patent No. US20010012831A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09768,840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/206,499

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36, 749
 REFERENCE/DOCKET NUMBER: PF-0261 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1035 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: CONTU01
 CLONE: 2509570
 78-09-768-R40-2

Alignment Scores:	6.74e-183	Length:	1055
Pred. No.:	1772.00	Matches:	328
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Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
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RESULT 2

US-09-847-809A-2
; Sequence 2, Application US/09847809A
; Patent No. US20020081604A1
; GENERAL INFORMATION:

APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Lal, Preeti
Corley, Neil C.

Shah, Purvi
TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: Pharmaceutics, Inc.

ADDRESSEE: Incyte Pharmaceuticals
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 NUMBER: US/09/847,809A

APPLICATION NUMBER: US/09/847,809A

FILING DATE: 01-May-2001
 CLASSIFICATION: <Unknown>

CLASSIFICATION: UNCLASSIFIED
PRIOR APPLICATION DATA:
CLASSIFICATION NUMBER: 09/270.270

APPLICATION NUMBER: 09/270,278
FILING DATE: 1999-03-16

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.

NAME: Billings, Lucy S.
REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0338 US
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166

TELEFAX: 650-845
TELEX: <Unknown>

FORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 1463 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: lin

IMMEDIATE SOURCE:
LIBRARY: RATRNOT02

CLONE: 922578
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US-09-847-809A-2

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RESULT 3

US-09-905-291A-220

Sequence 220, Application US/09905291A

Patent No. US20020160374A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/905,291A

CURRENT FILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/30999

APPLICANT: WILLIAMS, I. MARCEL
 APPLICANT: WOOD, WILLIAM, I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACID ENCODING THE SAME


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: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: PRIOR FILING DATE: 2000-01-05
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: TYPE: DNA
: ORGANISM: Homo Sapien
US-09-902-853-220

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Best Local Similarity:
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DB:             100.00%
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Gaps:           0
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Dd		215	GGACGGGAATGCCARGAAATTGCACAACCTACCCACAGAGAAAGCAGGCCCTCTGT	274
Oy		81	GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerLeuAla	100
Dd		275	GGCGCGGATCGTGGACCGCATGACCGCGGGGACCGCCACCGCTGGGTGTGGCTGGCC	334
Oy		101	GluLeuArgAlaTyrIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla	120
Dd		335	GAGCTTCGCGGTGGATCGCCACACCGCACCGCACATACGGACTCGGTGAGCGCG	394
Oy		121	AlaThrAspThrTyrAspThrAspArgAspGlyArgValGlyTrpGluLeuArgasn	140
Dd		395	GCCTGGGACAGTACGACACGGACCGCGCGCGTGTGGTGGAGAGGTCGCGCAAC	454
Oy		141	AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr	160
Dd		455	GCCACCTATGCCCACTACGCGCCCGGTGAAGAATAATTCATGAGCTGGAGGATGCAGAGCC	514
Oy		161	TyrLysLysMetLeuAlaArgAspGluArgArgPheArgValAlaAspGlnAspGlyAsp	180
Dd		515	TACAAAAGATGTGCTCGGACGACGCGCTTTCGCGGTGGCCGACGAGATGGGGAC	574
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Dd		575	TCGATGGCCACTCGAGAGGAGCTGACAGCCTTCTCTGCACCCGAGAGTTCCTCATCATG	634
Oy		201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220
Dd		635	CGGACATCTGATTGCTGAACCCCTGGAGGACCTGGACAGAACAAAGATGCTATGTC	694
Oy		221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla	240

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Db	755	TGGGTGCACAGCAGGAGAGCAGCAGCTCCGGGACTTCGGGGATCTGAAACAAGGATGGGCAC	814
Qy	261	LeuAspGlySerGluValGlyHisTrpValLeuProPheAlaGlnAspGlnProLeuVal	280
Db	815	CTGGATGGGAGTGGAGTGGGCCACTGGGTCTCGCCCTGCCAGGACCAAGCCCTTGGTG	874
Qy	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	875	GAAGCAACACCACTGCTGCACGAGAGCGACACGAAAGGATGGCGCTGTGACAAAGCG	934
Qy	301	GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTrpGlyGluAsp	320
Db	935	GAATCTCTGGGTAAATTGGAAACATGTTTGTGGCGAGTCAGGCCACCAACTATGGCAGGAC	994
Qy	321	LeuThrArgHisAspGluLeu	328
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; Publication No. US20020197671A1			
GENERAL INFORMATION:			
; APPLICANT: Genentech, Inc.			
; APPLICANT: Ashkenazi, Avi			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, A.			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, Christopher J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth, J.			
; APPLICANT: Kijavlin, Ivar J.			
; APPLICANT: Macher, Jennie P.			
; APPLICANT: Pan, James			
; APPLICANT: Peoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William, I.			
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
FILE OF INVENTION: Acids Encoding the Same			
FILE REFERENCE: 10466-14			
CURRENT APPLICATION NUMBER: US/09/907,824			
CURRENT FILING DATE: 2001-07-17			
PRIOR APPLICATION NUMBER: 09/665,350			
PRIOR FILING DATE: 2000-09-18			
PRIOR APPLICATION NUMBER: PCT/US00/04414			
PRIOR FILING DATE: 2000-02-22			
PRIOR APPLICATION NUMBER: US 60/143,048			
PRIOR FILING DATE: 1999-07-07			
PRIOR APPLICATION NUMBER: US 60/145,698			
PRIOR FILING DATE: 1999-07-26			
PRIOR APPLICATION NUMBER: US 60/146,222			
PRIOR FILING DATE: 1999-07-28			
PRIOR APPLICATION NUMBER: PCT/US99/20594			
PRIOR FILING DATE: 1999-09-08			
PRIOR APPLICATION NUMBER: PCT/US99/20944			
PRIOR FILING DATE: 1999-09-13			
PRIOR APPLICATION NUMBER: PCT/US99/21090			


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, PRIOR FILING DATE: 1999-09-15
, PRIOR APPLICATION NUMBER: PCT/US99/21547
, PRIOR FILING DATE: 1999-09-15
, PRIOR APPLICATION NUMBER: PCT/US99/23089
, PRIOR FILING DATE: 1999-10-05
, PRIOR APPLICATION NUMBER: PCT/US99/28214
, PRIOR FILING DATE: 1999-11-29
, PRIOR APPLICATION NUMBER: PCT/US99/28313
, PRIOR FILING DATE: 1999-11-30
, PRIOR APPLICATION NUMBER: PCT/US99/28564
, PRIOR FILING DATE: 1999-12-02
, PRIOR APPLICATION NUMBER: PCT/US99/28565
, PRIOR FILING DATE: 1999-12-02
, PRIOR APPLICATION NUMBER: PCT/US99/30095
, PRIOR FILING DATE: 1999-12-16
, PRIOR APPLICATION NUMBER: PCT/US99/30911
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US99/30999
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US00/00219
, PRIOR FILING DATE: 2000-01-05
, NUMBER OF SEQ ID NOS: 423
, SEQ ID NO 220
, LENGTH: 1503
, TYPE: DNA
, ORGANISM: Homo Sapien
, rs-09-907-824-220

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Alignment Scores:	1.05e-182	Length:	1503
Pred. NO.:	1772.00	Matches:	338
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:	9		

US-09-907-824-220 (1-1503)

[illegible][illegible]

RESULT 6

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RESOLUTION 907-841-220
Sequence 220, Application US/09907841
Publication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Truncated Acidic Polypeptides
TITLE OF INVENTION: Acids Encoding Peptides
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/9907841
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: PCT/US00/009078
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/141414
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/141414

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: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 220
: LENGTH: 1503
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-907-841-230

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Alignment Scores:	
Pred. No.:	1.05e-182
Score:	1772.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	9
Length:	1503
Matches:	328
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-768-840-1 (1-328) x US-09-907-841-220 (1-1503)

[illegible]


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1  PRIOR APPLICATION NUMBER: PCT/US99/20594
2  PRIOR FILING DATE: 1999-09-08
3  PRIOR APPLICATION NUMBER: PCT/US99/20944
4  PRIOR FILING DATE: 1999-09-13
5  PRIOR APPLICATION NUMBER: PCT/US99/21090
6  PRIOR FILING DATE: 1999-09-15
7  PRIOR APPLICATION NUMBER: PCT/US99/21547
8  PRIOR FILING DATE: 1999-09-15
9  PRIOR APPLICATION NUMBER: PCT/US99/23089
10 PRIOR FILING DATE: 1999-10-05
11 PRIOR APPLICATION NUMBER: PCT/US99/28214
12 PRIOR FILING DATE: 1999-11-29
13 PRIOR APPLICATION NUMBER: PCT/US99/28313
14 PRIOR FILING DATE: 1999-11-30
15 PRIOR APPLICATION NUMBER: PCT/US99/28564
16 PRIOR FILING DATE: 1999-12-02
17 PRIOR APPLICATION NUMBER: PCT/US99/28565
18 PRIOR FILING DATE: 1999-12-02
19 PRIOR APPLICATION NUMBER: PCT/US99/30095
20 PRIOR FILING DATE: 1999-12-16
21 PRIOR APPLICATION NUMBER: PCT/US99/30911
22 PRIOR FILING DATE: 1999-12-20
23 PRIOR APPLICATION NUMBER: PCT/US99/30999
24 PRIOR FILING DATE: 1999-12-20
25 PRIOR APPLICATION NUMBER: PCT/US00/00219
26 PRIOR FILING DATE: 2000-01-05
27 NUMBER OF SEQ ID NOS: 423
28
29 SEQ ID NO 220
30 LENGTH: 1503
31 TYPE: DNA
32 ORGANISM: Homo Sapien
33
34 HS-09-904-011-220

```

Alignment Scores:	1.05e-182	Length:	1503
Pred. No.:	1772.00	Matches:	328
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:	9		

US-00-769-840-1 (1-328) X US-09-904-011-220 (1-1503)

[illegible]

Db	455	CCCACTATGCCCACTACGCGCGGTGAAGAAATTCATGACGTGGAGGATGCAGAGCC	514
Qy	161	TyrlLysMetLeuLaarGaspGluArqArqPheAqValaLaAspGlnAspGlyasp	180
Db	515	TACAAAAGATGCTGGCTGGGACGAGCGCGTTTCGGGTGGCCGACCAAGATGGGAC	574
Qy	161	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
Db	575	TCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGGAGTTCCTCACATG	634
Qy	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220
Db	635	CGGGACATCGGTGCTGTAACCCCTGGAGGACCTGCAGACAACAAAGATGGCTATGTC	694
Qy	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla	240
Db	695	CAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCGCTGGGAGGAGGAGCGCGC	754
Qy	241	TrpValGlnThrGluArqGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	755	TGGGTGCAGACGGAGAGCGACAGCTTCGGGACTTCGGGATCTGAACAAGGATGGGCAC	814
Qy	261	LeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal	280
Db	815	CTGATGGGAGTGAGGTGGCGCACCTGGGTGCTGCCCTGCCACGAGCAGCCCTGGTG	874
Qy	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	875	GAGGCCACACCACTGCTGCACGAGAGGCACACGACGAAGGATGGCGGCTGAGCAAGCG	934
Qy	301	GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
Db	935	GAATCTCGGGTAATTGGAACATGTTGTGGGACGTAGGCCACCAACTATGGCGAGGAC	994
Qy	321	LeuThrArgHisAspGluLeu	328
Db	995	CTGACCGCGGACCACCATGAGCTG	1018
RESULT 8			
US-10-028-072-363			
; Sequence 363, Application US/10028072			
; Publication No. US20030004311A1			
GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Beresini, Maureen			
; APPLICANT: DeForge, Laura			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Flavaro, Ellen			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Sherwood, Steven			
; APPLICANT: Smith, Victoria			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Watanabe, Colin K			
; APPLICANT: Wood, William			
; APPLICANT: Zhang			
TITLE OF INVENTION:			
FILE REFERENCE:			
CURRENT APPLICATION NUMBER: US/10/028,072			
CURRENT FILING DATE: 2001-12-19			
PRIOR APPLICATION NUMBER: 60/049911			
PRIOR FILING DATE: 1997-06-18			
PRIOR APPLICATION NUMBER: 60/056974			
PRIOR FILING DATE: 1997-08-26			
PRIOR APPLICATION NUMBER: 60/059113			
PRIOR FILING DATE: 1997-09-17			
PRIOR APPLICATION NUMBER: 60/059115			
PRIOR FILING DATE: 1997-09-17			
PRIOR APPLICATION NUMBER: 60/059117			

DEPT. 8

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US-10-028-072-363
; Sequence 363, Application US/10028072
; Publication No. US20030004311A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
;
; TITLE OF INVENTION:
;
; FILE REFERENCE:
;
; CURRENT APPLICATION NUMBER: US/10/028, 072
; CURRENT FILING DATE: 2001-12-19
;
; PRIOR APPLICATION NUMBER: 60/049911
;
; PRIOR FILING DATE: 1997-06-18
;
; PRIOR APPLICATION NUMBER: 60/056974
;
; PRIOR FILING DATE: 1997-08-26
;
; PRIOR APPLICATION NUMBER: 60/059113
;
; PRIOR FILING DATE: 1997-09-17
;
; PRIOR APPLICATION NUMBER: 60/059115
;
; PRIOR FILING DATE: 1997-09-17
;
; PRIOR APPLICATION NUMBER: 60/059117
;

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201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnIysAspGlyTyrVal 220

US-09-768-840-1 (1-328) x US-09-906-742-220 (1-1503)

RESULT 10

[illegible]

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Db	395	GCCTGGGACACGTACGACACGAGCCGCGCGGTGTGGAGGAGCTCGCGAAC	454
Qy	141	AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr	160
Db	455	GCCACCTATGCCCACTTCGCGCCCGGTGAAGAAATTCATGACGTGGAGGATGCAGAGCC	514
Qy	161	TyrtysLysMetLeuAlaArgAspGluArgArgPheArgValAlaAspGlnAspGlyAsp	180
Db	515	TACAAAGAATGCTGGCTCGGACGAGCGGCTTCCTCGGCTGCCACCAGGATGGGGAC	574
Qy	181	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
Db	575	TCGATGGCCACTCGAGAGAGCTGACAGCCTTCCTGCAACCCGAGGAGTTCCTCCACATG	634
Qy	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220
Db	635	CGGGACATCGTGATTCGTGAACCCCTGGAGGACCTGCACAGAAACAAAGATGGCTATGTC	694
Qy	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluLuproAla	240
Db	695	CAGGTGGAGGAGTACATCGCGATCTCTACTCAGCCGACCCCTGGGAGGAGGCGCGCG	754
Qy	241	TrpValGlnThrGluAIGGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	755	TGGGTGCAGACGGAGAGCGCAGCTCCGGGACTCTCCGGGATCTCAACAAGGATGGCCAC	814
Qy	261	LeuAspGlySerGluValGlyHisTyrPValLeuProProAlaGlnAspGlnProLeuVal	280
Db	815	CTFGATGGGAGTAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACCCCTGGGTG	874
Qy	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	875	GAAGCCAAACCACTGCTGCACGAGAGCGACCGAAGGATGGCGGCTGAGCAAGCG	934
Qy	301	GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
Db	935	GAATCTCGGTAAATGGAAACATGTTGTGGGCAGTCAGGCCAACCACTATGCGAGGAC	994
Qy	321	LeuThrArgHisAspGluLeu	328
Db	995	CTGACCGCGCACCATGATGAGCTG	1018

RESULT 12

US-10-140-470-363
: Sequence 363, Application US/10140470
: Publication NO. US20030022331A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: ACIDS ENCODING THE SAME
: CURRENT APPLICATION NUMBER: P3330R1C160
: CURRENT FILING DATE: 2002-05-06
: Prior Application removed - See PaIm or File Wrapper
: NUMBER OF SEQ ID NOS: 550

[illegible]

[illegible]

Search completed: May 19, 2003, 13:54:20
Job time : 222 secs

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GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 12:17:36 ; Search time 57 Seconds
(without alignments)
1764.736 Million cell updates/sec

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Perfect score: 1772
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB-Issued_Patents_NA -QFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MAYFLX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09768840 -CGN 1 1 40 -runat_14052003_095558_16069 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA.*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length	ID	Description
1	1772	100.0	1055	2	US-08-828-242-2
2	1772	100.0	1055	4	US-09-206-499-2
3	1772	100.0	1463	4	US-08-910-927B-2
4	1772	100.0	1463	4	US-09-270-270-2
5	1693	95.0	1490	4	US-09-484-970B-53
6	842.5	47.5	2658	2	US-08-910-927B-4
7	842.5	47.5	2658	4	US-09-270-270-4
8	456.5	25.8	954	2	US-08-535-722-1
9	456.5	25.8	954	4	US-09-384-301-1
10	391	22.1	1192	1	US-08-840-683-1
11	255	14.4	1992	4	US-09-484-970B-150
12	136.5	7.7	1496	3	US-09-048-889-9

13	128	7.2	1400	1	US-08-464-164-1
14	128	7.2	1400	1	US-08-338-057-1
15	128	7.2	1400	2	US-08-668-416-1
16	124.5	7.0	853	3	US-08-963-409-2
17	122.5	6.9	2456	3	US-08-813-150-5
18	118	6.7	1929	2	US-08-818-253-1
19	118	6.7	1929	4	US-08-818-252-1
20	118	6.7	1929	2	US-08-818-253-3
21	118	6.7	1929	4	US-08-818-252-3
22	115	6.5	1929	2	US-08-818-253-5
23	115	6.5	1929	4	US-08-818-252-5
24	115	6.5	1971	2	US-08-818-253-7
25	115	6.5	1971	4	US-08-818-252-7
26	113.5	6.4	1859	4	US-09-399-913-23
27	113.5	6.4	1859	4	US-09-399-913-23
28	111	6.3	1247	4	US-09-399-913-15
29	111	6.3	1247	4	US-09-298-731-15
30	111	6.3	1401	4	US-09-239-905-1
31	110.5	6.2	2191	4	US-09-399-913-25
32	110.5	6.2	2191	4	US-09-298-731-25
33	109.5	6.2	1349	1	US-07-951-715A-20
34	109.5	6.2	1349	2	US-08-459-448A-20
35	109.5	6.2	1349	3	US-08-459-504B-20
36	109.5	6.2	1349	3	US-08-459-504B-20
37	109.5	6.2	1349	3	US-08-459-444-20
38	109.5	6.2	1349	4	US-09-547-422-20
39	108.5	6.1	50937	4	US-09-428-517-1
40	108	6.1	2343	4	US-09-399-913-17
41	108	6.1	2343	4	US-09-298-731-17
42	107.5	6.1	2009	4	US-09-399-913-13
43	107.5	6.1	2009	4	US-09-298-731-13
44	107	6.0	906	1	US-08-100-874-1
45	106.5	6.0	1904	4	US-09-399-913-29

ALIGNMENTS

RESULT 1
US-08-828-242-2
; Sequence 2, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goll, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc..
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166

Qy	128	AspArgAspGlyArgValGlyTrpGluGluLeuArgAsnAlaThrTyrGlyHisTyrAla	147
Db	460	AATGAGGACGGCGCTGTTTCTCGGAGGAGTATAAAATGCCACTACGCTACGTTTGA	519
Qy	148	ProGlyGluGluPheHisAspValGluAspAlaGluThrTyrLysLysMetLeuAlaArg	167
Db	520	-----GATGATCCAGATCCTCATCGATGGATTTAACTATAACAGATGATGGTTAGA	570
Qy	168	AspGluArgArgPheArgValAlaAspGlnAspGlyAspSerMetAlaThrArgGluGlu	187
Db	571	GATGAGCGAGGTTTAAATGGCACAAGAGTATGAGACCTCATTTGCCACCAAGGAGGAG	630
Qy	188	LeuThrAlaPheLeuHisProGluGluPheProHisMetArgAspIleValIleAlaGlu	207
Db	631	TTCCACAGCTTCTCGACCCCTCAGGAGTATGACTACATCAAAAGATATAGTAGTACAGAA	690
Qy	208	ThrLeuGluAspLeuAspArgAsnLysAspGlyTyrValGlnValGluGluLysIleAla	227
Db	691	ACAATGGAAGATATAGATAAGAATGCTGATGGTTTCATTCATGCTAGAGAGCATATTGGT	750
Qy	228	AspLeuTyrSerAlaGluProGlyGluGluGluProAlaThrValGlnThrGluArgGln	247
Db	751	GACATGTACAGCCATCATGGGAATACTGATGAGCCAGAAATGGGTAAAGACAGAGCGAG	810
Qy	248	GlnPheArgAspPheArgAspLeuAsnLysAspGlyHisLeuAspGlySerGluValGly	267
Db	811	CAGTTTGTTCGGGATATAGAACCGGTGATGGGAAGATGGACAGAGACGACCAAA	870
Qy	268	HisTrpValLeuProAlaGlnAspGlnProLeuValGluAlaAsnHisLeuHis	287
Db	871	GACTGGATCTCTCCCTCAGACTATGATCATGCAGAGGACGACAGCCAGCCCTGGTCTAT	930
Qy	288	GluSerAspThrAspLysAspGlyArgLeuSerLysAlaGluIleLeuGlyAsnTrpAsn	307
Db	931	GAATCAGACCAAAACAAGGATGGCAAGCTTACCAAGGAGGAGATCGTTGCACAGTATGAC	990
Qy	308	MetPheValGlySerGlnAlaThrAsnTyrGlyGluAspLeuThrArgHisHisAsp	326
Db	991	TTATTTTGTGGCAGCCAGCCACAGATTTTGGGAGCCCTTAGTACGGATGATGAG	1047

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1 RESULT 7
2 US-09-270-270-4
3 ; Sequence 4, Application US/09270270
4 ; Patent No. 6235477
5 ; GENERAL INFORMATION:
6 ; APPLICANT: Bandman, Olga
7 ; APPLICANT: Hillman, Jennifer L.
8 ; APPLICANT: Lal, Preeti
9 ; APPLICANT: Corley, Neil C.
10 ; APPLICANT: Shah, Purvi
11 ; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
12 ; NUMBER OF SEQUENCES: 6
13 ; CORRESPONDENCE ADDRESS:
14 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
15 ; STREET: 3174 Porter Drive
16 ; CITY: Palo Alto
17 ; STATE: CA
18 ; COUNTRY: USA
19 ; ZIP: 94304
20 ; COMPUTER READABLE FORM:
21 ; MEDIUM TYPE: Diskette
22 ; COMPUTER: IBM Compatible
23 ; OPERATING SYSTEM: DOS
24 ; SOFTWARE: Fastseq for Windows Version 2.0
25 ; CURRENT APPLICATION DATA:
26 ; APPLICATION NUMBER: US/09/270,270
27 ; FILING DATE:
28 ; CLASSIFICATION:
29 ; PRIOR APPLICATION DATA:
30 ; APPLICATION NUMBER: 08/910,927
31 ; FILING DATE:
32 ; ATTORNEY/AGENT INFORMATION:

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[illegible]

[illegible]

Qy 317 TyrGlyGluaspLeuThrArg-----HisHisAspGluLeu 328
D6 785 TATGCACAGACAGCTCCATGATGACTATTTCTATCATCATGAGCTT 829

RESULT 11
US-09-484-970B-150
; Sequence 150, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484, 970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 150
; LENGTH: 1992
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 232513.3
; NAME/KEY: unsure
; LOCATION: 1421
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-150

Alignment Scores:
Pred. No.: 7,33e-18 Length: 1992
Score: 255.00 Matches: 87
Percent Similarity: 41.96% Conservative: 67
Best Local Similarity: 23.71% Mismatches: 158
Query Match: 14.39% Indels: 55
Gaps: 12
DB: 4

US-09-768-840-1 (1-328) x US-09-484-970B-150 (1-1992)

Qy 3 TrpArgProSer-----ValLeuLeuLeuLeu 11
D6 319 TGGCGTCCAGGTGGGGTCCCTCATTTGGCTCGCTCGCTCGCTCGCTCGGG 378
Qy 12 LeuLeuLeuArgHisGlyAlaGlnGlyProSerProAspAlaGlyProHisGlyGln 31
D6 379 GCAGTCTCTTGATGGAGCGGTCTGCAGCGCTGCCAACCACTCGTCCACT-----CGA 432
Qy 32 GlyArgValHisGlnAlaAlaProLeuSerAspAlaProHisasp-----46
D6 433 GAGAGAGTACCAACAGGAGGAGAGAGTATGATCTCGTCCGCCACAGCACCTGAGCGGGTG 492
Qy 47 -----AspAlaHisGlyAsnPhenGlnTyrAspHisGlnAlaPheLeuGlyArg 62
D6 493 AAGCTGAGATGGAGCGGCACCTCAATCGCGCTCCACAGGAGGCTTCTCTAGGCAAG 552
Qy 63 GluValAlaLysGluPheAspGlnLeuThrPro-----GluGluSerGlnAlaArg 79
D6 553 GACCTGGGTGGCTTTGATGAGGAGCGGAGCGGCGGAGCGAGGAGTATGATGTCAT 612
Qy 80 Leu-GlyArgIleValAspArgMetAspArgAlaGlyAspGlyTrpValSerLe 99
D6 613 CTTTCCAGGTGGATGTGAACACTGACCCGGAAG-----ATCAGTGC 654
Qy 99 uAlaGluLeuArgAlaTrpIleAlaHisThrGlnAlaHisIleArgAspSerVal 119
D6 655 CAAGGAGATGCAGCGCTGGATCATCGAAGAGCGGCCGAGCACTTCCAGGAGGCCATGGA 714
Qy 119 rAlaAla-----TrpAspThrTyrAspThrAspArgAspGlyArgValGlyTrpG 136
D6 715 GGAGAGCAACACACACTTCCCGCGCGTGGAGCCCTGACGGGACGGTACGTGCTTGGGA 774

Qy 136 uGluLeuArg-----AsnAlaThrTyrGlyHisTyrAlaProGlyGluGluPheHi 153
D6 775 CGAGTATTAAGTGAAGTTTGGCGAGTAAGGCCAT-----AGCGAGAGAGGAGTTGC 828
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D6 829 CGACGCCATCAGGCTCAACAGGAACTCAAAGTGGACGAGGAGAAACACAGGAAGTCTTGA 888
Qy 165 uAlaArgaspGluArgArgPheArgValAlaAspGlnAspGlyAspSerMetalaThrAr 185
D6 889 GAACCTGAAGGACCCCTGGTACCAGCGGACAGCCCTCCAGACCTGCTGCTGACGGA 948
Qy 185 gGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMetArgAspIleVal 205
D6 949 GGAGGAGTTCCTGTCTGCTCCACCCGAGCAGCACCGCGGGAATGCTCAGGTTTCATGGT 1008
Qy 205 eAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrValGlnValGluGluTy 225
D6 1009 GAAGGAGATCGTCCGGGACCTGGACGAGGCGGTGACCAAGCAGCTCTCTGTGCCGAGTT 1068
Qy 225 rIleAla-----AspLeuTyrSerAlaGluProGlyGluGlu---GluProAlaTr 241
D6 1069 CATCTCCCTGCCGTGGGACCCGTGGAGAACACGAGCGGCGGACACATTGACCAACTG 1128
Qy 241 pValGlnThrGluArgGlnPheArgAspPheArgAspLeuAsnLysAspGlyHisLe 261
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Qy 261 uAspGlySerGluValGlyHisTrpValLeuProAlaGlnAspGlnProLeuValG 281
D6 1189 GACCGCGGAGGAGCTGGAGAGCTACATGGACCCCTGAACGAGTACACGCCCTGAACGA 1248
Qy 281 uAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAlaGl 301
D6 1249 GGCCACAGCATGATCGCTCGCCGACGAGAACACACACACACACCTGGAGCCCGAGGA 1308
Qy 301 uIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAspLe 321
D6 1309 GTGCTCAAGTACAGCGAGTTCTTACCGGCGCAAGCTGTGTGCTACGCGCGAGCGGT 1368
Qy 321 uThrArgHisAspGlu 327
D6 1369 G-----CACGAGGAG 1378

RESULT 12
US-09-048-889-9
; Sequence 9, Application US/09048889
; Patent No. 6117989
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lal, Preeti
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: HUMAN CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/048,889
; FILING DATE: Herewith
; CLASSIFICATION:

us-09-768-840-1.p2n.rni

Tue May 20 14:43:25 2003

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Organon Teknika Corporation
STREET: 1330 Piccard Drive
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,057
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93.309078.9
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Eimeria maxima
STRAIN: Houghton
DEVELOPMENTAL STAGE: sporozoite
IMMEDIATE SOURCE:
LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
CLONE: Em70-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1368
US-08-338-057-1

Alignment Scores:
Pred. No.: 0.000184 Length: 1400
Score: 128.00 Matches: 42
Percent Similarity: 40.12% Conservative: 25
Best Local Similarity: 25.15% Mismatches: 70
Query Match: 7.22% Indels: 30
DB: Gaps: 5

US-09-768-840-1 (1-328) x US-08-464-164-1 (1-1400)
QY 70 GlnLeuThrProGluGluSerGlnAlaArgLeuGlyArgIleValAspArgMetAspArg 89
Db 883 AAATTAACAACAATGAGGAGACACGACGAATTAATAAAATCTCCAGAGATGGATAAG 942
QY 90 AlaGlyAspGly-----AspGlyTrpValSerLeuAlaGlu 101
Db 943 AACGGAGACGCAACTCGATTAACAAGAAATTAATGAGGGGTATGTTCAATTAATGAAG 1002
QY 102 LeuArgAlaTrp---IleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla 120
Db 1003 CTAAGAAGGAGAGATGTTCTCTATTAACAAGAGTGAATTAAGAGAGAGAGTGAACAA 1062
QY 121 AlaTrpAspThrTyrAspThrAspArgAspGlyArgValGlyTrpGluGluLeuArgAsn 140
Db 1063 GTTCTTGAGGCTGTAGACTTCGATGAAGATGATTTATTAATATTCAGATTC----- 1116
QY 141 AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160
Db 1117 -----GTGACGGTGGCAATGGAT 1134
QY 161 TyrLysLysMetLeuAlaArgAsp-----GluArgArgPheArgValAlaAlaAspGlnAsp 178
Db 1135 AGAAGAAGCTGTATATCAAGACAAAGACTTGAAGAGCATTGAGATGTTGACTCGGAT 1194
QY 179 GlyAspSerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPhePro 198
Db 1195 GGATFCAGGAATAATCTCTCTCTGATTAAGTACTATATTTGGTGTAAAGCGAG----- 1248
QY 199 HisMetArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGly 218
Db 1249 ---TTAGACTCGGAGGATGCGCTCGGTATTAGCAAGATGATGCAATAATATGACGGA 1305
QY 219 TyrValGlnValGluGluTyr 225
Db 1306 GAAGTTGACTTTGAGGAATTT 1326

RESULT 14
US-08-338-057-1
; Sequence 1, Application US/08338057
; Patent No. 5795741
; GENERAL INFORMATION:
; APPLICANT: Tomley, Fiona M.
; APPLICANT: Dunn, Paul P. J.
; APPLICANT: Bumstead, Janene M.
; APPLICANT: Vermeulen, Arno N.
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 10

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Db 1117 -----GTGACGGTGGCAATGAT 1134
 Qy 161 TyrLysLysMetLeuAlaArgAsp-----GluArgArgPheArgValAlaAspGlnAsp 178
 Db 1135 AGAAGAACTCTGTTATCAAGACAAGACTTGAAGAGAGATTGCGAGATGTTCCGACTCGGAT 1194
 Qy 179 GlyAspSerMetAlaThrArgGluGluThrAlaPheLeuHisProGluGluPhePro 198
 Db 1195 GGATCAGAGAAAATCTCTCTCTGAATAGCTACTATATTGGTGTAAAGCGAG----- 1248
 Qy 199 HisMetArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGly 218
 Db 1249 ---TTAGACTCGGAGGATGCGCGGTATTAGCACAAGTTGATCGAATATATGACCGA 1305
 Qy 219 TyrValGlnValGluGluTyr 225
 Db 1306 GAAGTTGACTTTGAGGAATTT 1326

RESULT 15
 US-08-668-416-1
 ; Sequence 1, Application US/08668416
 ; Patent No. 5843722
 ; GENERAL INFORMATION:
 ; APPLICANT: Tomley, Fiona M.
 ; APPLICANT: Dunn, Paul P. J.
 ; APPLICANT: Bumstead, Janene M.
 ; APPLICANT: Vermeulen, Arno N.
 ; TITLE OF INVENTION: Coccidiosis poultry vaccine
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS: 10
 ; ADDRESSEE: Akzo No. 5843722el Patent Department
 ; STREET: 1300 Piccard Drive, Suite 206
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: U.S.A.
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/668,416
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/464,164
 ; FILING DATE: June 2, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gormley, Mary E.
 ; REGISTRATION NUMBER: 34,409
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 258-5200
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1400 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: C-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Eimeria maxima
 ; STRAIN: Houghton
 ; DEVELOPMENTAL STAGE: sporozoite
 ; IMMEDIATE SOURCE:
 ; LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
 ; CLONE: Em70-1
 ; FEATURE:
 ; NAME/KEY: CDS

LOCATION: 1..1368
 US-08-668-416-1
 Alignment Scores:
 Pred. No.: 0.000184 Length: 1400
 Score: 128.00 Matches: 42
 Percent Similarity: 40.12% Conservative: 25
 Best Local Similarity: 25.15% Mismatches: 70
 Query Match: 7.22% Indels: 30
 DB: 2 Gaps: 5
 US-09-768-840-1 (1-328) x US-08-668-416-1 (1-1400)
 Qy 70 GlnLeuThrProGluGluSerGlnAlaArgLeuGlyArgIleValAspArgMetAspArg 89
 Db 883 AAATTAACAACAATGAGGAGACAGACGAAATTAATAAATCTTCAGAAAGATGATGAAG 942
 Qy 90 AlaGlyAspGly-----AspGlyTrpValSerLeuAlaGlu 101
 Db 943 AACGGAGACGGACAACCTCGATAACAAGAAATTAATGGAGGGTTATGTTGAATTAATGAAG 1002
 Qy 102 LeuArgAlaTrp---IleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla 120
 Db 1003 CTAAAGAGGAAGATGTTCTCTATTAGACAAGAGTGCATTTGACACAGAAGTTCAACAA 1062
 Qy 121 AlaTrpAspThrTyrAspThrArgAspGlyArgValGlyTrpGluGluLeuArgAsn 140
 Db 1063 GTTCTTGAGGCTGTAGACTTCGATAAGAATGATTTATTAATATTCAGAAATTC----- 1116
 Qy 141 AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160
 Db 1117 -----GTGACGGTGGCAATGAT 1134
 Qy 161 TyrLysLysMetLeuAlaArgAsp-----GluArgArgPheArgValAlaAspGlnAsp 178
 Db 1135 AGAAGAACTCTGTTATCAAGACAAGACTTGAAGAGAGATTGCGAGATGTTCCGACTCGGAT 1194
 Qy 179 GlyAspSerMetAlaThrArgGluGluThrAlaPheLeuHisProGluGluPhePro 198
 Db 1195 GGATCAGAGAAAATCTCTCTCTCTGTAATAGCTACTATATTGGTGTAAAGCGAG----- 1248
 Qy 199 HisMetArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGly 218
 Db 1249 ---TTAGACTCGGAGGATGCGCGGTATTAGCACAAGTTGATCGAATATATGACCGA 1305
 Qy 219 TyrValGlnValGluGluTyr 225
 Db 1306 GAAGTTGACTTTGAGGAATTT 1326

Search completed: May 19, 2003, 13:50:41
 Job time : 75 secs

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GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 12:17:01 ; Search time 1715 Seconds
(without alignments)
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Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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37	956	54.0	954	9	AL573989	AL573989 AL573989
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41	939.5	53.0	1989	11	AK017494	AK017494 Mus muscu
42	934	52.7	555	10	AV723508	AV723508 AV723508
43	922	52.0	572	12	BO888768	BO888768 H3157C12-
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
AL544155 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI020YC22 5
prime, mRNA sequence.
ACCESSION
AL544155
VERSION
AL544155.1
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1092)
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization

FEATURES
SOURCE

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i. lili
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5750333"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
/notes="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Stanford). Research Genetics tracking code 026. Note:

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BASE COUNT	238 a	318 c	392 g	162 t	1 others
ORIGIN	this is a NIH_MGC Library."				

Alignment Scores:

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Score:	1654.00	Matches:	316
Percent Similarity:	96.99%	Conservative:	6
Best Local Similarity:	95.18%	Mismatches:	6
Query Match:	93.34%	Indels:	4
DB:	14	Gaps:	0

US-09-768-840-1 (1-328) x BM920379 (1-1111)

[illegible]

Qy	300	laGluLeuLeuGlyAsnTrpAsnMetPhe-ValGlySerGlnAlaThrAsnTyrGly-Gl	319
Db	949	CGGAATCCTGGGTAAATTGGAACATGTTTGGGGGGCAGTCACCCACCACAATATGGCCGA	1008
Qy	319	wASPLEuthrArgHisHisAspGluLeu	328
Db	1009	GGACTGACCCCGGAACCAACCAATGAGGTG	1036
RESULT	3		
LOCUS	AL520513	1005 bp	mRNA
DEFINITION	AL520513.LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB006YC08 5 prime, mRNA sequence.	linear	EST 13-FEB-
ACCESSION	AL520513		
VERSION	AL520513.1	GI:12784006	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1005)		
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.		

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i./organism="Homo sapiens"
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/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT3
was primed with a NotI-oligo (dT) P
enriched, double-stranded cDNA was
cloned into the Not I and Eco RV s
vector. Library was normalized. I
by Life Technologies. Contact : F
Technologies, a division of Invitro
Drive Rockville, Maryland 20850, U
8371 Email : fliang@lifetech.com U
http://fulllength.invitrogen.com"

```

BASE COUNT	221 a	250 c	359 g	150 t	25 others
ORIGIN	http://fulllength.invitrogen.com*				

Alignment Scores:	
Pred. No.:	1,41e-152
Score:	1479.00
Length:	1005
Matches:	291
Conservative:	7
Mismatches:	27
Indels:	4
Gaps:	1
DB:	9

US-09-768-840-1 (1-328) x AL520513 (1-1005)

[illegible]


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Db 959 AACAAAGGGGAAATCCCGGGGAACCTGGGAACATGTTTGGGG 1004

RESULT 6
B1820206 824 bp mRNA linear EST 04-OCT-2001
LOCUS 603037040F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178104 5',
DEFINITION mRNA sequence.
ACCESSION B1820206
VERSION B1820206.1 GI:15931756
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 824)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: crabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1A011443 row: p column: 09
High quality sequence stop: 801.
Location/Qualifiers
1..824
/organism="Homo sapiens"
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/note="Organ: pooled brain, lung, testis; Vector:
PCMV-SPT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
BASE COUNT 180 a 227 c 298 g 119 t
ORIGIN

Alignment Scores:
Pred. No.: 5,59e-146 Length: 824
Score: 1418.00 Matches: 270
Percent Similarity: 98.5% Conservative: 1
Best Local Similarity: 98.18% Mismatches: 3
Query Match: 80.02% Indels: 2
DB: 13 Gaps: 0

US-09-768-840-1 (1-328) x B1820206 (1-824)

QY 42 AspAProHisAspAspAlaHisGlyAsnPhcGlnTyAspHisGluAlaPheLeuGly 61
|||||
Db 2 GAGCGTCCCATGATGACGCCACGGGAACCTCCAGTACGACCATGAGGCTTCCCTGGGA 61
QY 62 ArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeuGly 81
|||||
Db 62 CGGGAAGTGGCCAGGAAATTCGACCAACTACCCCGAGAGAAAGCCGCGCTGCGGG 121
QY 82 ArgTleValAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerLeuAlaGlu 101
|||||
Db 122 CGGATCGTGACCGCATGACCGCGCGGGGACGCGGCTGGGTGTGCTGGCGCGAG 181
QY 102 LeuArgAlaTrpIleAlaHisThrGlnGlnArgHisTleArgAspSerValSerAlaAla 121
|||||

```


vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filang@lifetech.com URL : <http://fulllength.invitrogen.com>

```

BASE COUNT
ORIGIN
180 a 241 c 324 g 129 t 9 others
      http://fulllength.invitrogen.com"

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Alignment Scores:

Pred. No.:	5,39e-145	Length:	883
Score:	1409.50	Matches:	277
Percent Similarity:	98.23%	Conservative:	0
Best Local Similarity:	98.23%	Mismatches:	4
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DB:	9	Gaps:	0

US-09-768-840-1 (1-328) x AL543374 (1-883)

[illegible]

Db	821	-CTGGATGGGAGTAGGTT-GGSCACTGGTGTGCC-CCTGCCCAGGAMCAGCCCCCTGGT	877
QY	280	lGlu 281 	
Db	878	GGAA 881	
RESULT	8		
AL543274			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			

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/clone="CS0DI001YN23"  
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/tissue_type="placenta"
/note="vector: ncwvsnorm c.

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was primed with a NotI-oligo

enriched, double-stranded c

cloned into the Not I and EcoRI vector. Library was normally

Life Technologies. Contact

a division of Invitrogen 98

Rockville, Maryland 20850, USA
Email : flanagan@fifetech.com

<http://fulllength.invitrogen.com>

BASE COUNT	176 a	235 c	306 g	128 t
ORIGIN				

Alignment Scores:

Pred. No.:	1.66e-138	Length:
Score:	1250.50	

Percent Similarity: 95.34%

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Query Match: 76.21%
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Gap:

US-09-768-840-1 (1-328) x AL543274 (1-852)

Ov

MetMetTnphrproDroscivlfroutanyant - P

[illegible]

Db 20 ATGATGTGGCGACCATCAGTTCTGCTGCTTCTGTTGCTA

21 [vsProseProse] "Cl...a...a..."

11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 10

dbb 80 AAGCCATCCCCAGACGCAGGCCCTCATGGCCAGGGGAGG

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db 140 AGCGACGCTCCCCATGATGACGCCACGGGAAGTCCAG

67 GlyArgGluValAlaIleuGluProMetGluLeuMetLeu

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81 G[VArgI]evAl AsnArgMetAsnAsnMetAl ArgMetMetAl

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Marchionni, L., Mashima, J., Mazzearelli, J., Mombearts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
111217851

5 (bases 1 to 1112)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Baldaracci, T., Baldaracci, R., Bono, H., Brownstein, M., Bult, C., Carlinici, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Onizuka, K., Otsu, M., Ozaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, R., Sakai, K., Sakai, K., Sano, H., Sasaki, D., Saigo, H., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toyota, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9216, fax: 81-45-503-9216)

Release visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

DATA library was prepared and sequenced in Mouse Genome encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer 5' GAGAGAGAGCGCGCACTGAGTGTGTTTTTTTTTNN 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0. Second strand cDNA was prepared with the primer adapter of sequence 5' GAGAGAGAGAGATCCAGAGCTCAATTAATTAATTAACCCCCC 3'. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

Location/Qualifiers

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Db 343 GAGCTCCGCGCGTGTATGCGGCACACAGCAGCGGCACATCCGTGACTCGGTGAGCGCA 402
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QY 141 AlaThrTyArgHisTyAlaProGlyGluGluPheHisAspVal-GluAspAlaGluTh 160
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ACCESSION BI903868
VERSION BI903868.1 GI:16165963
KEYWORDS EST
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 867)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonald, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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 Location/Qualifiers
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FEATURES
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 BASE COUNT 200 a 232 c 292 g 143 t
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 Query Match: 73.02% Indels: 1
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US-09-768-840-1 (1-328) x BI903868 (1-867)

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 QY 106 IleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAlaAlaTrpAspThr 125
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 Db 305 GCTCGGATGAGCGCGGATTCGGGTAGCGACCAAGATGGGACTCATGGCTACTCGG 364
 QY 186 GluGluLeuThrAlaPheLeuHisProGluPheProHisMetArgAspIleValLe 205
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BASE COUNT			
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Pred. No.:			
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Percent Similarity:			
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US-09-768-840-1 (1-328) x BQ885637 (1-914)			
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Tue May 20 14:43:26 2003

tracking code 036." 152 t

BASE CO
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ПС-09-768-840-1 (1-328) x BM543703 (1-1082)

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Job time : 1729 secs

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 12:14:45 ; Search time 294 Seconds
(without alignments)
2512.433 Million cell updates/sec

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Fgapop 6.0, Fgapext 7.0
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Searched: 2185239 seqs, 1125999159 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1772	100.0	1503	21	AAV58589	Human PRO272 prote
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20	944	53.3	2104	24	ABK64404	Colon adenocarcino
21	944	53.3	2358	22	AAV72801	Human cervical can
22	857.5	48.4	948	22	ABK35607	Gene encoding nove
23	857.5	48.4	948	22	ABK35607	Human cDNA sequenc
24	842.5	47.5	945	19	AAV29034	Open reading frame
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28	842.5	47.5	3311	19	AAV29033	Human protein comp
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31	833.5	47.0	2459	22	AAV94764	Human full-length
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33	672	37.9	3697	23	ABL01940	Drosophila melanog
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35	570.5	32.2	760	22	AAV05350	Human cDNA clone (
36	537	30.3	300	20	AAV214539	Human gene express
37	530.5	29.9	644	21	AAV43519	Mouse secreted exp
38	523.5	29.5	595	22	AAV93410	CDNA encoding SRT
39	516.5	29.1	701	23	ABV24771	Human prostate exp
40	489	27.6	352	20	AAV40251	Human secreted pro
41	465	26.2	1365	23	ABL14859	Drosophila melanog
42	456.5	25.8	954	18	AAV73913	E6-binding protein
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ALIGNMENTS

RESULT 1

AAV57600
ID AAV57600 standard; cDNA; 1055 BP.

XX AC AAV57600;

XX DT 15-DEC-1998 (first entry)

XX DE Human calcium-binding protein encoding cDNA.

XX KW HCBP; beta thalassemia; cell proliferation; cancer; adenocarcinoma;
XX KW leukemia; lymphoma; melanoma; sarcoma; ss.

XX OS Homo sapiens.

XX FT Key Location/Qualifiers

XX CDS 34..1020

[illegible]

P-PSDB; AAB33424.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

Claim 23; Fig 21; 309pp: English.

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO for proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic chronic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary and Whipple's disease, bowel disease, gluten-sensitive enteropathy and allergic diseases, autoimmune or immune-mediated skin diseases, transplantation associated immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

Human PRO272 protein UNQ239 encoding cDNA SEQ ID NO:50.

Human: immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthopathy; Sjogren's syndrome; thyroiditis; idiopathic inflammatory myopathy; autoimmune haemolytic anaemia; diabetes mellitus; systemic vasculitis; autoimmune thrombocytopenia; immune-mediated renal disease; autoimmune thrombocytopenia; hepatobiliary disease; Whipple's disease; demyelinating bowel disease; gluten-sensitive enteropathy; inflammatory bowel disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease; graft rejection; graft-versus-host-disease; ss.

XX DE Homo sapiens.

XX OS WO2000053758-A2.

XX PN 14-SEP-2000.

XX PD

XX PF 02-MAR-2000; 2000WO-US05841.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 10-MAR-1999; 99US-0123618.

XX PR 12-MAR-1999; 99US-0123957.

XX PR 13-MAR-1999; 99US-0125775.

XX PR 12-APR-1999; 99US-0128849.

XX PR 20-APR-1999; 99WO-US08615.

XX PR 28-APR-1999; 99US-0131445.

XX PR 04-MAY-1999; 99US-0132371.

XX PR 14-MAY-1999; 99US-0134287.

XX PR 02-JUN-1999; 99WO-US12252.

XX PR 23-JUN-1999; 99US-0141037.

XX PR 20-JUL-1999; 99US-0144758.

XX PR 26-JUL-1999; 99US-0145698.

XX PR 28-JUL-1999; 99US-0146222.

XX PR 01-SEP-1999; 99WO-US20111.

XX PR 08-SEP-1999; 99WO-US20594.

XX PR 13-SEP-1999; 99WO-US20944.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 05-OCT-1999; 99WO-US21547.

XX PR 29-OCT-1999; 99US-0162506.

XX PR 29-NOV-1999; 99WO-US28214.

XX PR 30-NOV-1999; 99WO-US28313.

XX PR 30-NOV-1999; 99WO-US28409.

XX PR 01-DEC-1999; 99WO-US28301.

XX PR 01-DEC-1999; 99WO-US28634.

XX PR 02-DEC-1999; 99WO-US28551.

XX PR 02-DEC-1999; 99WO-US28564.

XX PR 16-DEC-1999; 99WO-US30095.

XX PR 20-DEC-1999; 99WO-US31274.

XX PR 30-DEC-1999; 99WO-US00219.

XX PR 05-JAN-2000; 2000WO-US00277.

XX PR 06-JAN-2000; 2000WO-US00376.

XX PR 11-FEB-2000; 2000WO-US03565.

XX PR 18-FEB-2000; 2000WO-US04341.

XX PR 18-FEB-2000; 2000WO-US04342.

XX PR 22-FEB-2000; 2000WO-US04414.

XX PR

XX PA (GETH) GENENTECH INC.

XX PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

XX PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

XX PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX PR WPI: 2000-572271/53.

PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
XX P-PSDB; AAU12353.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical
XX
PS Claim 3; Fig 363; 813pp; English.
XX
CC AAS21244-AAS21518 encode for novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
SQ Sequence 1503 BP; 357 A; 456 C; 474 G; 216 T; 0 other;

XX Homo sapiens.
OS WO200104311-AI.
PN
XX 18-JAN-2001.
PD
XX 22-FEB-2000; 200OWO-US04414.
PF
XX 07-JUL-1999; 99US-0143048.
PR
XX 26-JUL-1999; 99US-0145698.
PR
XX 28-JUL-1999; 99US-0146222.
PR
XX 08-SEP-1999; 99WO-US20594.
PR
XX 13-SEP-1999; 99WO-US20944.
PR
XX 15-SEP-1999; 99WO-US21090.
PR
XX 15-SEP-1999; 99WO-US21547.
PR
XX 05-OCT-1999; 99WO-US23089.
PR
XX 29-NOV-1999; 99WO-US28214.
PR
XX 30-NOV-1999; 99WO-US28313.
PR
XX 16-DEC-1999; 99WO-US30095.
PR
XX 20-DEC-1999; 99WO-US30911.
PR
XX 20-DEC-1999; 99WO-US30999.
PR
XX 05-JAN-2000; 99WO-US00219.
PA

XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Botstein D, Desnovers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen KE, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kiljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPI: 2001-081051/09.
DR P-PSDB; AAB80250.
DR
XX sixty one nucleic acids encoding PRO polypeptides which are useful in
PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
PT Alzheimer's disease)
XX
XX Claim 2; Fig 79; 393pp; English.
PS
XX The present sequence is one of sixty one nucleic acids encoding novel
CC secreted and transmembrane PRO polypeptides. The PRO polypeptides are
CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
CC squamous cell carcinoma), gastrointestinal disorders (e.g.
CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
CC Parkinson's disease), wound repair, cardiovascular disorders (e.g. asthma,
CC endometrial bleeding angiogenesis, ischaemias such as coronary
CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
CC diabetes and retinal disorders such as retinitis pigmentosum.
CC The PRO nucleic acids have applications in molecular biology, including
XX use as hybridization probes, and in chromosome and gene mapping.
XX
XX Sequence 1503 BP; 357 A; 456 C; 474 G; 216 T; 0 other;
SQ

Alignment Scores:
Pred. No.: 1,35e-152 Length: 1503
Score: 1772.00 Matches: 328
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps:

US-09-768-840-1 (1-328) x AAF72411 (1-1503)

QY 1 MetMetTtPArgProSerValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuGly 20
Db 35 ATGATGTGGCGACCATCAGTTCTGCTGCTACTGCAGGCACGGGCCACGGG 94
QY 21 LysProSerProAspAlaGlyProHisGlyGlnGlyArgValHisGlnAlaAProLeu 40

Db 95 AAGCCATCCCGACGAGCGCCCTCATGCCAGGGAGGGTGCACACGAGCGGCCCCCTGTG 154
 Qy 41 SerAspAlaProHisAspAspAlaHisGlyAsnPhelNtyrAspHisGluAlaPheLeu 60
 Db 155 AGCGAGCTCCCATATGATGACGCCCGCCCGGAACTTCCAGTAGCAGCATGAGCTTTCCTG 214
 Qy 61 GlyArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeu 80
 Db 215 GGACGGGAAGTGCCAAAGAAATTCGACCAACTCACCCAGAGGAAGCAGCGCGTCTG 274
 Qy 81 GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTyrPValSerLeuAla 100
 Db 275 GGCGGATCGTGACCGCATGACCGCGCGGGGAGCGGCGGCTGGTGTCTGCTGCGCC 334
 Qy 101 GluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla 120
 Db 335 GAGCTTCGCGCGTGGATCGGCACACGCGAGCGGCGACATACGGGCTCGGTGAGCGCG 394
 Qy 121 AlaTrpAspThrTyrAspThrAspArgAspGlyArgValGlyTyrPValGluLeuArgAsn 140
 Db 395 GCGTGGGACACGTACGACCGGACCGCGGCGGCTGTGGTGGAGGAGCTGCGCAAC 454
 Qy 141 AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisaspValGluAspAlaGluThr 160
 Db 455 GCGACCTATGGCCACTACGCGCGCGCGTGAAGAAATTCATGCGTGGAGATGCAGAGACC 514
 Qy 161 TyrLysLysMetLeuAlaArgAspGluArgArgPheArgValAlaAlaAspGlnAspGlyAsp 180
 Db 515 TACAAAAGATGCTGGCTCGGAGGAGCGGCGTTCGCGGTGGCCGACGAGGATGGGAC 574
 Qy 181 SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
 Db 575 TCGATGGCCACTCGAGAGGAGCTGACAGCGCTTCTGACCCCGGAGGATTCCTCACATG 634
 Qy 201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal 220
 Db 635 CGGACATCGTGTGATGCTGAACCCCTGGAGGAGCTGGACAGAAACAAAGATGCTATGTC 694
 Qy 221 GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla 240
 Db 695 CAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGCGGCTGGGAGGAGGCGCGG 754
 Qy 241 TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis 260
 Db 755 TGGTGCAGACGAGGAGGAGGAGGAGTTCGCGGACTTCGCGGATCTGAACAAGATGGGCAC 814
 Qy 261 LeuAspGlySerGluValGlyHisTyrPValLeuProProAlaGlnAspGlnProLeuVal 280
 Db 815 CTGGATGGGAGTGAGTGGCGGCTGGTGTGCTGCCCCCTGCCCCAGGACGCGCCCTGTG 874
 Qy 281 GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla 300
 Db 875 GAAGCCCAACCACTGCTGCACGAGAGCGACAGGACAGGATGGCGGCTGAGCAAGAGCG 934
 Qy 301 GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp 320
 Db 935 GAAATCTCGGTAAATGACACATGTTGTGGGCACTGTCAGGCCACCACTATGGCGAGGAC 994
 Qy 321 LeuThrArgHisHisAspGluLeu 328
 Db 995 CTGACCCGCGCACCGATGAGCTG 1018
 RESULT 8
 AAC97455
 ID AAC97455 standard; cDNA; 1503 BP.
 XX
 AC AAC97455;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Human angiogenesis-associated protein PRO272 cDNA, SEQ ID NO:112.
 XX
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;

KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal; ag.
 XX
 OS Homo sapiens.
 XX
 PN WO200053753-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 05-JAN-2000; 2000WO-US00219.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 XX
 (GETH) GENENTECH INC.
 XX
 PA Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
 XX
 DR WPI: 2001-090793/10.
 XX P-PSDB; AAB53085.
 PT
 PS New isolated nucleic acid for producing a PRO polypeptide, analyzing
 XX genetic disorders and treating cardiovascular, endothelial or
 XX angiogenic disorders, such as atherosclerosis, wounds or cancer -
 XX
 PS Claim 58; Fig 43; 293pp; English.
 XX
 CC The invention relates to novel human angiogenesis-associated proteins
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 CC PRO proteins. The invention also relates to vectors and host cells
 CC comprising a PRO nucleic acid, the recombinant production of a PRO
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
 CC compounds which inhibit the expression of a PRO gene. The invention
 CC additionally encompasses methods of identifying modulators of PRO
 CC expression or activity; diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting
 CC mutations in a PRO gene, or the expression level of a PRO gene within a
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 CC administration of a PRO protein, or an agonist or antagonist thereof.
 CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
 CC agonists and PRO antagonists may be used as therapeutic agents to treat
 CC cardiovascular, endothelial or angiogenic disorders, such as
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
 CC disease, or stroke. PRO nucleic acids are additionally useful in the
 CC recombinant production of PRO proteins, as hybridisation probes to
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,

Db	721	CGGGACATCGTGATTGCTGTAACCCCTGGAGACCTGGACAGAAACAANGATGGCTATGTC	780
Qy	221	GlnValGluGluTyrIleLeuAspLeuTyrSerIlaGluProGlyGluGluGluProAla	240
Db	781	CAGGTGGAGAGTACATCGCGGATCTGTACTCAGCCGAGCTCGGAGGAGGAGCGCGG	840
Qy	241	TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	841	TGGGTGCAGACGAGGAGGACACGATCCGGGACTTCGGGATCTGAACAAGGATGGCAC	900
Qy	261	LeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal	280
Db	901	CTGGATGGGAGTGGAGTGGGCCACTGGGTGCTCCCCCTGCCCGAGCCAGCCCTGGTG	960
Qy	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	961	GAAGCCAACCACTGCTGTGCACAGGAGGCGACCGGCAAGGATGGCGGTGTAGCAAAAGC	1020

QY 301 GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaIleThrArg⁹⁰TrpGlyGluAsn 320

[illegible]

	Qy	321	LeuThrArgHisHisAspGluLeu	328	
	Db	1081	CTGACCCGGCACCACCATGAGCTG	1104	
<hr/>					
RESULT 10					

AA000656
ID AA000656 standard; DNA; 1507 bp.

[illegible]

PT and for rational drug and therapy design, comprises detecting at least
PT one differentially expressed gene product -
XX
PS
XX Claim 42: Page 105-106; 135pp; English.

The present invention relates to methods for detecting a cancerous colon cell involving detecting at least one differentially expressed gene such as those given in AAL41595-AAL41611. This is useful for diagnosing colon cancer, in rational drug and therapy design, and for identifying additional genes linked to the development or inhibition of development of colon cancer. Examples of colon cancer which can be detected include adenomatous polyp, colorectal carcinoma, high metastatic potential colon tumours and metastatic colon cancer. The present sequence is a colon cancer associated protein coding sequence.

SQ Sequence 1507 BP; 350 A; 456 C; 479 G; 213 T; 9 other;

Alignment Scores:		
Prod. No.:	4.77e-152	Length:
Score:	1766.00	Matches:
Percent Similarity:	99.70%	Conservative:
Best Local Similarity:	99.70%	Mismatches:
Query Match:	99.66%	Indels:
DB:	24	Gaps:
		0
		0
		1507
		327

US-09-768-840-1 (1-328) x AAL41601 (1-1507)

OY

MetMetTTrArgProSerValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuHISGlyAlaLaGlnCly 20
|||||
D6

ATGATGTGGCCACCATCAGTTCTGCCTTCGTGCTACTCAGCACCGGGGCCAAGGG 113
|||||

QY 21 LysProSerProAspAlaGlyProHisGlyGlnGlyArgValHisGlnAlaAlaProLeu 40
|||
114 RAGCCATCCCCAGACGAGGCCCTCATGCCAGGGAGGGTGCCACGAGGGGCCCCCTG 173
Db

Qy 41 SerAspAlaProHisAspAspAlaHisGlyAsnPheGlnTyrAspHisGluAlaPheLeu 60
|||||
Db 174 AGCGACGCTCCCATGATGACGCCACGGGAACCTCCAGTACGACCATGAGGCTTTTCCTG 233
Ov 174 AGCGACGCTCCCATGATGACGCCACGGGAACCTCCAGTACGACCATGAGGCTTTTCCTG 233

[illegible]

294 GGGCGGATCTGGACGCATGACCGCGGGGGACGGCCAGCGCTGGGTGCTGGCC 353

Ddb
 354 GAGCTTCGCGCGTGGATCGGCACACGACGACGCGGCACATACGGGACTCGGTGAGCGCG 413
 121 AlaTrpAspThrTrpAspThrAspArgAspG.VargValGltTrpGlnGlnLeuArgSer. 140

db 414 GCCTGGGACACGTACGACACGACCGCGACGGCGCTGTGGTGGGAGAGCTGGCGCAC 473

dy 141 AlaThrTyrClyHisTyrAlaProClyClnuPheHisAspValGlnuAspAlaGluThr 160

db 474 GCCACCTATGGCCACTAGCGCCCGGTGAAGATTTCATGACGTGGAGGATCCAGAGACC 533

yy 161 TyrLysLysMetLeuAlaArgAspCiluaArgGpheArgValAlaAspClnAspGlyAsp 180

534 TACAAAGATCTGGCTGGGACAGCGCGTTTCGGGTGGCCGACACGATGGGAC 593

181 SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200

594 TCGATGCCCACTCGAGAGAGAGCTGACAGCCTTCCTCACCCGAGGAGTTCCTCCACATG 653

654 CGSGACATCGTATTGCTGTAACCCCTGGAGACCCTGGACAGAAACAAGATGGCTATGTC 713

221 GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla 240

Db	714	CAGTGGAGGAGTACATCGGGGATCTCTACTCAGCCGAGCCTGGGGAGGAGGAGCCGGCG	773
Qy	241	TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	774	TGGGTGCAGACGGAGAGCGACAGTTCGGGGACTTCGGGGATCTGAACAAAGATGGGCAC	833
Qy	261	LeuAspGlySerGluValGlyHisTrpValLeuProAlaGlnAspGlnProLeuVal	280
Db	834	CTGATGGGAGTAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGACCAGCCCTGGTG	893
Qy	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	894	GAAGCCAACCACCTGCTGCACGARACGGACAGGACAGGATGGGCGGTGACAAAGCG	953
Qy	301	GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
Db	954	SAANTCTGGGTAAATTGGAAACATGTTGTGGGCAGTCAGGCCCAACCACTATGGYGAGGAC	1013
Qy	321	LeuThrArgHisAspGluLeu	328
Db	1014	CTGACCGGCACCAACCATGAGCTG	1037

RESULT 12

AA41603
ID AAL

XX
15.241003 32400810, CDNA; 1307 BP.AC
XX
AAL41603;DT 19-APR-2002 (first entry)
vv

Human colon cancer related

XX CT : ON at Macaouches Ennace
XX
KW Human: color correct: anti-static

human, colon cancer; cytostatic; drug design; adenomatous polyp;
 colorectal carcinoma; cytostatic; drug design; adenomatous polyp;
 metastatic colon cancer; high metastatic potential colon tumour;
 metastatic colon cancer; gene; ss.

XX
SO
Homo sapiensXX
name appears;

PN
XX
WO200196523-A2.

PD
XX
20-DEC-2001.

PF 15-JUN-2001; 2001WO-US19313.

XX
PR 15-JUN-2000: 2000US-211835P[illegible]PA
(CHLR) CHIRON CORP.
XX

Kennedy GC, Kang S, Reinhard C, Jefferson AB;

DR WPI; 2002-164362/21.

Detecting a cancerous colon cell, useful for diagnosing colon cancer
 and for rational drug and therapy design, comprises detecting at least
 one differentially expressed gene product -

Claim 42; Page 107; 135pp; English.

The present invention relates to methods for detecting a cancerous colon cell involving detecting at least one differentially expressed gene such as those given in AAU41595-AAU41611. This is useful for diagnosing colon cancer, in rational drug and therapy design, and for identifying additional genes linked to the development or inhibition of development of colon cancer. Examples of colon cancer which can be detected include adenomatous polyp, colorectal carcinoma, high metastatic potential colon tumours and metastatic colon cancer. The present sequence is a colon cancer associated protein coding sequence.

Sequence 1507 BP; 350 A; 456 C; 479 G; 213 T; 9 other;

Alignment Scores:

red. No. :
core.

core: 1/66.00 Matches:

Percent Similarity:	99.70%	Conservative:	1
Best Local Similarity:	99.70%	Mismatches:	0
Query Match:	99.66%	Indels:	0
DB:	24	Gaps:	0

MS-09-768-840-1 (1-328) x AAL41603 (1-1507)

[illegible]

1014 CTGACCCGGCACCACGATGAGCTG 1037

RESULT 13

AAI63890 1480 bp.

XX
AC
AAT63890:

AC
XX
DT

Human polynucleotide SEO ID NO 98.

Human polyneuritic disease

XX	Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW	immunoprotective; nontropic; neuroprotective; antibacterial; virucide
KW	fungicide; ophthalmologic; cytostatic; immunosuppressive; nontropic;
KW	antiproliferative; antitumor; antidiabetic;
KW	antiinflammatory; antileukemic; hepatotropic; anticonvulsant; antibacterial;
KW	antiparasitic; cardiac; gene therapy; cancer; immune disorder;
KW	cardiovascular disorder; neurological disease; infection; human; ss.

XX Homo sapiens.
OS

XX
PN WQ200155308-A2:

PD 02-AUG-2001.

17-JAN-2001: 2001WO-US01309.

21 - JAN-2000: 2000US-0179065

PR	31-JAN-2000;	2000US-0180628
PR	04-FEB-2000;	2000US-0180628

PR 24-FEB-2000; 2000US-0184004
PR 02-MAR-2000; 2000US-0186350

PR 16-MAR-2000; 2000US-0189874
PR 17-MAR-2000; 2000US-0190076

PR 18-APR-2000; 2000US-0198123
PR 19-MAY-2000; 2000US-0205515

PR 13 MAR 2000 2000US-0209467
PR 07-JUN-2000; 2000US-0214886
PR 29 JUN 2000; 2000US-0214886

PR 28-JUN-2000; 2000US-0215135
PR 30-JUN-2000; 2000US-0215135

PR	07 - JUL - 2000;	2000US - 0216847
PR	07 - JUL - 2000;	2000US - 0216880
PR	07 - JUL - 2000;	2000US - 0216880

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PR 30-AUG-2000; 2000US-0228925

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 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2000US-0254097.
 PR 05-JAN-2001; 2000US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI: 2001-488781/53.
 P-PSTDB; AAM43584.

New isolated nucleic acids and polypeptides, useful for diagnosing,
treating and/or preventing human diseases and disorders -
Claim 1; SEQ ID NO 98; 664pp + Sequence Listing; English.

The invention relates to human polynucleotides (AAI63803-AAI64012) and
the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
or ameliorating medical conditions e.g. by protein or gene therapy. The
genes were isolated from a range of human tissues disclosed in the
specification. The nucleic acids, proteins, antibodies and (antagonists)
are useful in the diagnosis, treatment and prevention of: (a) cancer,
e.g. breast and ovarian cancer and other cancers of the adrenal gland,
bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
urogenital; (b) immune disorders e.g. Addison's disease, allergies,
autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
colitis; (c) cardiovascular disorders such as myocardial infarction;
(d) wound healing; (e) neurological disorders such as cerebral palsy and
epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
and parasitic infections.

Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 1480 BP; 329 A; 458 C; 479 G; 214 T; 0 other;

Tue May 20 14:43:25 2003

us-09-768-840-1.p2n.rng

QY	61	GlyArgGluValAlaIysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeu	80	OS	Homo sapiens.
DB	227	GGACGGGAAGTGCCCAAGAAATTCGACCAACTTCACCCAGAGGAAGCCAGGCCGCTCTG	286	XX	WO200155304-A2.
QY	81	GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerLeuAla	100	XX	02-AUG-2001.
DB	287	GGCGGATCGTGACCGCATGACCGCGCGGGGAGCGCGACCGCTGCTGCTGGCC	346	XX	17-JAN-2001; 2001WO-US01302.
QY	101	GluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla	120	XX	31-JAN-2000; 2000US-0179065.
DB	347	GAGCTTCGCGGTGATCGGCACACGACGCGGACATACGGGACTTCGGTGAGCGCG	406	PR	04-FEB-2000; 2000US-0184664.
QY	121	AlaTrpAspThrTrpAspThrAspArgAspGlyArgValGlyTrpGluGluLeuArgAsn	140	PR	02-MAR-2000; 2000US-0186350.
DB	407	GCCTGGGACACGTACGACACGGACCGCGCGGTGGGTGGGAGGAGCTGGCGAAC	466	PR	16-MAR-2000; 2000US-0189874.
QY	141	AlaThrTrpGlyHisTrpAlaProGlyGluGluPheHisAspValGluAspAlaGluThr	160	PR	17-MAR-2000; 2000US-0190076.
DB	467	GCCACCTATGCCCACTACGCGCGCGGTGGAAGAATTTTCATGACCTGGAGGATGCAGAC	526	PR	18-APR-2000; 2000US-0198123.
QY	161	TyrIysLysMetLeuAlaArgAspGluArgPheArgValAlaAlaAspGlnAspGlyAsp	180	PR	19-MAY-2000; 2000US-0205515.
DB	527	TACAAAAGATGCTGGCTCGGGACGCGCGGTTCGGGTGGCCGACCAAGGATGGGAC	586	PR	07-JUN-2000; 2000US-0209467.
QY	181	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200	PR	08-JUN-2000; 2000US-0214886.
DB	587	TCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGGAGTTCCTCACATG	646	PR	28-JUN-2000; 2000US-0215135.
QY	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220	PR	30-JUN-2000; 2000US-0216647.
DB	647	CGGGACATCGTGATTCGTAACCTTGAGGACCTGGAGGACCTGGACAGAACAAAGATGCTATGTC	706	PR	07-JUL-2000; 2000US-0216880.
QY	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla	240	PR	07-JUL-2000; 2000US-0217487.
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DB	767	TGGGTGCACACGAGGAGGAGGAGGAGTTCGGGACTTCGGGATCTGACACAGGATGGGCAC	826	PR	14-JUL-2000; 2000US-0220963.
QY	261	LeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal	280	PR	26-JUL-2000; 2000US-0220964.
DB	827	CTGGACGGAGTGAAGTGGCCACTGGTGTGCTGCCCTGCCAGGACCAAGCTGGTG	886	PR	26-JUL-2000; 2000US-0224518.
QY	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300	PR	14-AUG-2000; 2000US-0224519.
DB	887	GAAGCAACACCTGCTGCACGAGAGCGACACGGACAGGAGGCGCGCTGAGCAAGCG	946	PR	14-AUG-2000; 2000US-0225213.
QY	301	GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320	PR	14-AUG-2000; 2000US-0225214.
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PR	11-DEC-2000;	2000US-0251990.
PR	05-JAN-2001;	2001US-0254977.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	

XX	Rosen CA, Barash SC, Ruben SM;
PI	WPI; 2001-465568/50.
DR	P-PSDB; AAU19946.
XX	
PT	Isolated nucleic acid molecule encoding a calcium-binding protein is
PT	used in preventing, treating or ameliorating a medical condition -
XX	
PS	Claim 4; SEQ ID No 65; 542pp; English.
XX	
CC	The present invention relates to the isolation of novel human
CC	calcium-binding proteins (AAU19892-AAU19969), and cDNA and genomic
CC	sequences encoding for these proteins. The sequences of the invention
CC	are useful in the diagnosis, prevention and/or prognosis of diseases
CC	associated with aberrant calcium flux. Such disorders include
CC	neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
CC	immune dysfunction (e.g. severe combined immunodeficiency, SCID),
CC	digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
CC	disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
CC	infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
CC	novel calcium-binding proteins are also useful as screening tools to
CC	identify antagonists and/or agonists that may enhance or inhibit
CC	activities mediated by calcium-binding proteins. The polynucleotides of
CC	the invention are also useful in gene therapy. AAS31577-AAS31634
CC	represent cDNA sequences encoding for the novel human calcium-binding
CC	proteins.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
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Score:	1764.00 Matches: 327
Percent Similarity:	99.70% Conservative: 0
Best Local Similarity:	99.70% Mismatches: 1
Query Match:	99.55% Indels: 0
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Db	
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Oy	21 LysProSerProAspAlaGlyProHisGlyGlnGlyArgValHisGlnAlaProLeu 40
Db	107 AAGCCATCCCAGACGACGCCCTCATGCCAGGGGGGTGCACAGGCCGCCCGCTG 166
Oy	41 SerAspAlaProHisAspAspAlaHisGlyAsnPheGlnTyrAspHisGluAlaPheLeu 60
Db	167 AGCCAGCGCTCCCCATGATGACGCCACGGGAATCTCCAGTACGACCATGAGGCTTTCC 226
Oy	61 GlyArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeu 80
Db	227 GGACGGGAAGTGGCCAAGGAATTGCNACCACATCACCCAGAGGAAAGCCAGGCCCGCTG 286
Oy	81 GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerLeuAla 100
Db	287 GGGCGGATCGTGACCGCATGTGACCGCGCGGGGACGCGACGCGCTGGTGTCTCGTGGCC 346
Oy	101 GluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla 120
Db	347 GAGCTTCGCGCTGGATCCGCCACACAGCAGCGGGGCACATACGGGACTCGGTGACGCG 406
Oy	121 AlaTrpAspThrTyraSpThraspArgAspGlyArgValGlyTrpGluGluLeuArgAsn 140
Db	407 GCCTGGGACACGTAGCACACGACGCGCGCGCTGTGGGTGGAGGAGCTGCCCAAC 466
Oy	141 AlaThrTyrgLyHisTyraAlaproGlyGluclupheHisaspValGluAspAlaGluThr 160

us-09-768-840-1.1.p2n.rng

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QY 181 SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
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QY 201 ArgAspTleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal 220
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Db 707 CAGGTGGAGGATACATCGCGGATCTGTACTCAGCGAGCCTGGGGAGGAGGAGCGGCG 766
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Db 1007 CTGACCGCGCACCCAGATGAGCTG 1030

RESULT 15
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AC ABK43732;
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DT
DE
DE
XX
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200155318-A2.
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XX 02-AUG-2001.
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XX 17-JAN-2001; 2001WO-US01332.
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XX 31-JAN-2000; 2000US-0179065.
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PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
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PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
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PR 11-JUL-2000; 2000US-0217496.
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PR 26-JUL-2000; 2000US-0220963.
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PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
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Tue May 20 14:43:25 2003

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Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: May 19, 2003, 12:16:11 ; Search time 3395 Seconds
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Title: US-09-768-840-1

Perfect score: 1772

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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4	1772	100.0	1463	6	AR152960	Sequence AR152960
5	1772	100.0	1470	9	BC011346	Sequence BC011346
6	1772	100.0	1503	6	AX464230	Sequence AX464230
7	1766	99.7	1507	6	AX354366	Sequence AX354366
8	1766	99.7	1507	6	AX354369	Sequence AX354369
9	1759	99.3	1454	9	AF183423	Sequence AF183423
10	1645	92.8	1421	10	BC025602	Sequence BC025602
11	1596	90.1	1414	10	BC005487	Sequence BC005487
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ACCESSION	ARQ35969		
VERSION	ARQ35969.1 GI:5952637		
KEYWORDS	Unknown. Source ORGANISM		
REFERENCE	Unclassified.		
AUTHORS	Hillman,J.L.,and Goli,S.K.		
TITLE	Calcium-binding protein		
JOURNAL	Patent: US 5871970-A 2 16-FEB-1999;		
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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

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 ACCESSION AX354369
 VERSION AX354369.1 GI:18619211
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 SOURCE
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Kennedy,G.C., Kang,S., Reinhard,C. and Jefferson,A.B.
 TITLE Polynucleotides related to colon cancer
 JOURNAL Patent: WO 0196523-A.15 20-DEC-2001;
 CHIRON CORPORATION (US)
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 QY 41 SerAspAlaProHisAspAspAlaHisGlyAsnPhcGlnTyraSpHisGluAlaPheLeu 60
 Db 174 AGCACGCGTCCCCATGATGACGCCACCGGAACTCCAGTACGACCATGAGGCTTCCTG 233
 QY 61 GlyArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeu 80
 Db 234 GGACGGGAGTGGCCAGGAATTTCGACCAACTCACCCAGAGAAAAGCCAGGCCCGCTG 293
 QY 81 GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerLeuAla 100
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 QY 101 GluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla 120
 Db 354 GAGCTTCGCGCTGGATCCGGCACACGACGACGCGGACATACGGGACTCGGTGAGCGCG 413
 QY 121 AlaTrpAspThrTyraSpThrAspArgAspGlyArgValGlyTrpGluGluLeuArgAsn 140
 Db 414 GCCTGGGACACGTACGACACGACCGACCGCGCGCGGTGTGGGTGGGAGGAGCTGCGCAAC 473
 QY 141 AlaThrTyrglyHisTyralaproGlyGluPheHisAspValGluAspAlaGluThr 160
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 BASE COUNT
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QY	301	GlulLeuLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
Db	976	GAGATCTTGACCACTCGGAACATGTTGTGGCAGCCAGCCAGGCCACCACTACGGTGGAGAC	1035
QY	321	LeuThrArgHisHisAspGluLeu	328
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REMARK			
COMMENT			

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Series: IRAK Plate: 7 Row: h Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

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RESULT 12

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

REMARK

COMMENT

Alignment Scores: 1414
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DB 121 TAGGACCATGAGCGTCTCTGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 74 GluGluSerGlnAlaArgLeuGlyArgLeuValAspArgMetAspArgAlaGlyAspGly 93
DB 181 GAGGAAGCCAGCGCGACTTGGCGGATCGTAGACCGCATGGATCTTCTGGGAGCAGC 240
QY 94 AspGlyTrpValSerLeuAlaGluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHis 113
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QY 114 IleArgAspSerValSerAlaAlaTrpAspThrThrAspThrAspArgAspGlyArgVal 133
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DB 541 CCGGAGGAGTTCCTCATCATCGGGAGACATCGTGTAGCAGAGACCCCTGGAGGACCT 600
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QY 234 ProGlyGluGluGluProAlaTrpValGlnThrGluArgGlnGlnPheArgAspPheArg 253
DB 661 CTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 254 AspLeuAsnLysAspGlyHisLeuAspGlySerGluValGlyHisTrpValLeuProPro 273
DB 721 GATCTGAACAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 274 AlaGlnAspGlnProLeuValGluAlaAsnHisLeuLeuHisGluSerAspThrAspLys 293
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QY 294 AspGlyArgLeuSerLysAlaGluIleLeuGlyAsnTrpAsnMetPheValGlySerGln 313
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QY 314 AlaThrAsnTyrGlyGluAspLeuThrArgHisHisAspGluLeu 328

1454 bp mRNA linear PRI 12-JUL-2001
Homo sapiens, reticulocalbin 1, EF-hand calcium binding domain,
clone MGC:19541 IMAGE:3836263, mRNA, complete cds.
BC010120
BC010120 GI:14603329
MGC.
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1454)
Straussberg, R.
Direct Submission
Submitted (02-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, O.L., Masello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantiripop, S., Thomas, P.J.,
Tlongson, E.B., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 27 Row: i Column: 8
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 5419788.
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BASE COUNT 404 a 332 c 386 g 332 t
ORIGIN
Alignment Scores: 8.93e-56 Length: 1454
Pred. No.:


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QY 218 GlyTyrValGlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGlu 237
Db 713 GGGTTTGGATCAGGATGATATATTCGGATATGTTTCCATGAGGAGAAATGCGCCT 772
QY 238 GluProAlaThrValGlnThrGluArgGlnPheArgAspPheArgAspLeuAsnLys 257
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QY 258 AspGlyHisLeuAspGlySerGluValGlyHisTrpValLeuProAlaGlnAspGln 277
Db 833 GACGGAAGTTAGACAAAGATGAGATCGGCACCTGGATCTCCTCAAGATTATGATCAC 892
QY 278 ProLeuValGluAlaAsnHisLeuLeuSerAspThrAspLysAspGlyArgLeu 297
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QY 318 GlyGluAspLeuThrArgHisHisAspGluLeu 328
Db 1013 GGGGAAGATCTCACAAAATCATGATGAGCTT 1045

RESULT 14
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LOCUS Human mRNA for reticulocalbin, complete cds.
DEFINITION D42073
ACCESSION D42073
VERSION D42073.1 GI:1262328
KEYWORDS rcn; calcium binding protein; ER-hand protein; ER-resident protein;
reticulocalbin.
SOURCE Homo sapiens transitional carcinoma cell cell_line:BOY cDNA to
mRNA, clone:hr12 and hr19.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2104)
AUTHORS Ozawa,M.
TITLE Cloning of a human homologue of mouse reticulocalbin reveals
conservation of structural domains in the novel endoplasmic
reticulum resident Ca(2+)-binding protein with multiple EF-hand
motifs
JOURNAL J. Biochem. 117 (5), 1113-1119 (1995)
MEDLINE 96172582
REFERENCE 2 (bases 1 to 2104)
AUTHORS Ozawa,M.
TITLE Direct Submission
AUTHORS Submitted (10-NOV-1994) Masayuki Ozawa, Faculty of Medicine,
Kagoshima University, Department of Biochemistry; 8-35-1
Sakuragaoka, Kagoshima, Kagoshima 890, Japan (Tel:0992-75-5246,
Fax:0992-64-5618)
COMMENT On Apr 12, 1996 this sequence version replaced gi:575579.
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DB: 9 Gaps: 5
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QY 39 ProLeuSerAspAlaProHisAspAlaHisGlyAsnPheGlnTyrAspHisGluAla 58
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 QY 238 GluProAlaTTPValGlnThrGluArgGlnPheArgAspPheArgAspLeuAsnLys 257
 Db 773 GAGCCAGACTGGGTTTATACAGCGGAGCAGTTTAAAGAAATCCCGGATCTGAACAAG 832
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 QY 318 GlyGluAspLeuThrArgHisHisAspGluLeu 328
 Db 1013 GGGGAGATCTCAAAAAATCATGATGAGCTT 1045

RESULT 15
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 ACCESSION D13003
 VERSION D13003.1
 KEYWORDS ER-resident protein; calcium-binding protein; endoplasmic reticulum protein; multiple EF hand motifs; reticulocalbin.
 SOURCE Mus musculus (strain:129/Sv) teratocarcinoma cell_line:OTT6050 cDNA to mRNA, clone:O1 and M10.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Ozaawa.M. and Muramatsu.T.
 Reticulocalbin, a novel endoplasmic reticulum resident Ca(2+)-binding protein with multiple EF-hand motifs and a carboxyl-terminal HDL sequence
 J. Biol. Chem. 268 (1), 699-705 (1993)
 93107083
 2 (bases 1 to 1998)
 Ozaawa.M.
 Direct Submission
 Submitted (23-AUG-1997) Masayuki Ozaawa, Faculty of Medicine, Kagoshima University, Department of Biochemistry; 8-35-1 Sakuragaoka, Kagoshima, Kagoshima 890, Japan (Tel:0992-75-5246, Fax:0992-64-5618)
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 1568. 1573
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 1979. 1984
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 1998
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 545 a 412 c 543 g 498 t
 BASE COUNT
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 Query Match: 53.02% Indels: 16
 DB: 10 Gaps: 4

US-09-768-840-1 (1-328) x MUSRCAL (1-1998)
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 QY 35 SGlnAlaAlaProLeuSerAspAlaProHisAspAlaHisGlyAsnPheGlnTyrAs 55
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 QY 55 PHisGluAlaPheLeuGlyArgGluValAlaLysGluPheAspGlnLeuThrProGluG1 75
 Db 193 TCATGAGGCTTCCTGGCAAGGAGGACTCCAAGACCTTCGATCAGCTAAGCCGGACGA 252
 QY 75 USerGlnAlaArgLeuGlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspG1 95
 Db 253 GAGCAAGAGAGAGGCTGGGGAATTTGGATCGATCAGCTAAGCCGGACGA 306
 QY 95 YTrpValSerLeuAlaGluLeuArgAlaTTPileAlaHisThrGlnGlnArgHisLea1 115
 Db 307 CTTGTACTACTGAGGAGCTGAACTTTGGATCAACACGGGTACAGAAAAGATACATCTA 366
 QY 115 GAspSerValSerAlaAlaTTPAspThrTyrAspThrAspArgAspGlyArgValGlyTr 135
 Db 367 TGATAATGTCTAAAGTCTGGAAGGATTATGATAGGCAACAAAGATCTCCCTG 426
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 Db 427 GGAAGATACAGCAGCCACCTATGGCTACTACCTGGGAAACCCCGCTGAATTCATCA 486
 QY 154 pValGluAspAlaGluThrTyrLysLysMetLeuAlaArgAspGluArgArgPheArgVa 174
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 QY 194 oGluGluPheProHisMetArgAspIleValIleAlaGluThrLeuGluAspLeuAspAr 214
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us-09-768-840-1.p2n.rge

Tue May 20 14:43:25 2003

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Search completed: May 19, 2003, 13:20:51
 Job time : 3424 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2003, 10:40:07 ; Search time 103.883 Seconds
(without alignments)
650.575 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 1772
Sequence: 1 MMWRPSVLLLLLRHGAQG.....FVGSQATNYGDELTRHIDEL 328

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues 671580

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPREMBL21.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	1772	100.0	328	4 Q96D15	Q96d15 homo sapien
2	1759	99.3	328	4 Q9HB28	Q9hb28 homo sapien
3	1645	92.8	328	11 Q8R137	Q8r137 mus musculus
4	1596	90.1	315	11 Q99K35	Q99k35 mus musculus
5	1321	74.5	259	11 Q9CTD4	Q9ctd4 mus musculus
6	911	51.4	322	13 Q93434	Q93434 fugu rubrip
7	857.5	48.4	315	4 Q96RL3	Q96rl3 homo sapien
8	852	48.1	296	4 Q9NR43	Q9nr43 homo sapien
9	839.5	47.4	315	11 Q35783	Q35783 rattus norv
10	818	46.2	296	6 Q9MZ46	Q9mz46 sus scrofa
11	703.5	39.7	329	5 Q9SZK6	Q9szk6 drosophila
12	685	38.7	322	5 Q93136	Q93136 bombyx mori
13	639.5	36.1	314	5 Q23017	Q23017 caenorhabdi
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23	196.5	11.1	391	10 Q9FNN0	Q9fnn0 arabidopsis
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37	130	7.3	2439	5 Q9VSM2	Q9vsm2 drosophila
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43	128	7.2	414	5 Q24892	Q24892 elmeria max
44	127.5	7.2	271	4 Q96BK4	Q96bk4 homo sapien
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ALIGNMENTS

RESULT 1

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DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical 37.5 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
EL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013436; AAH13436.1; -;
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; EF-target.
DR Pfam; PF00036; ehand; 5
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
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KW Hypothetical protein.
SQ SEQUENCE 328 AA; 37493 MW; B64EDB28B9610B8D CRC64;

Query Match 100.0%; Score 1772; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.4e-124;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
QY 61 GREVAKEFDQLPEESQARLRGRVDRMDRAGDGDGWSVLAELRAVIAHTQORHIRDSVSA 120
DB 61 GREVAKEFDQLPEESQARLRGRVDRMDRAGDGDGWSVLAELRAVIAHTQORHIRDSVSA 120
QY 121 AWDYTDTRDGRGVGWEELRNATYGHVAPCEPHDYDAETVKKMLARDERFRVADQGD 180


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Db 121 AWDTYDTRDGRVGVWEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGVQVVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGVQVVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQOQFRDLNKGDLGSEVGHVWLPVPAQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WVQTERQOQFRDLNKGDLGSEVGHVWLPVPAQDQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328
Db 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328
RESULT 2
Q9HBZ8 PRELIMINARY; PRT; 328 AA.
AC Q9HBZ8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to hypothetical protein LOC57333.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HYPOTHALAMUS;
RA Peng Y., Gu Y., Huang C., Xu S., Han Z., Fu G., Chen Z.;
RT "A novel gene expressed in human hypothalamus.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF183423; AAG09692.1; -.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000886; EF-hand.
DR Pfam: PF00036; ehand; 4.
DR SMART: SM00054; EFh; 3.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE: PS00014; EF_TARGET; UNKNOWN_1.
SQ SEQUENCE 328 AA; 37424 MW; 9D23648795D3C670 CRC64;
Query Match 99.3%; Score 1759; DB 4; Length 328;
Best Local Similarity 99.4%; Pred. No. 1.3e-123;
Matches 326; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MMWRPSVLLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
Db 1 MMWRPSVLLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGVSLAELRAWTIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGVSLAELRAWTIAHTQQRHIRDSVSA 120
QY 121 AWDTYDTRDGRVGVWEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
Db 121 AWDTYDTRDGRVGVWEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGVQVVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGVQVVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQOQFRDLNKGDLGSEVGHVWLPVPAQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WVQTERQOQFRDLNKGDLGSEVGHVWLPVPAQDQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328
Db 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328
RESULT 3
Q9HBZ8 PRELIMINARY; PRT; 328 AA.
AC Q9HBZ8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to hypothetical protein LOC57333.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005487; AAH05487.1; -.
DR MGD: MGI:1915346; 6030455P07R1k.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000886; ER-target.
DR Pfam: PF00036; ehand; 4.
DR SMART: SM00054; EFh; 3.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE: PS00014; EF_TARGET; UNKNOWN_1.
SQ SEQUENCE 328 AA; 37973 MW; 913F5C6F0F88B316 CRC64;
Query Match 92.8%; Score 1645; DB 11; Length 328;
Best Local Similarity 92.7%; Pred. No. 4.3e-115;
Matches 304; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 1 MMWRPSVLLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
Db 1 MMWRPSVLLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGVSLAELRAWTIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGVSLAELRAWTIAHTQQRHIRDSVSA 120
QY 121 AWDTYDTRDGRVGVWEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
Db 121 AWDTYDTRDGRVGVWEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGVQVVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGVQVVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQOQFRDLNKGDLGSEVGHVWLPVPAQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WVQTERQOQFRDLNKGDLGSEVGHVWLPVPAQDQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328
Db 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328
RESULT 4
Q99K35 PRELIMINARY; PRT; 315 AA.
AC Q99K35;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to hypothetical protein LOC57333 (Fragment).
GN 6030455P07R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005487; AAH05487.1; -.
DR MGD: MGI:1915346; 6030455P07R1k.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000886; ER-target.
DR Pfam: PF00036; ehand; 4.
DR SMART: SM00054; EFh; 3.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE: PS00014; EF_TARGET; UNKNOWN_1.
SQ SEQUENCE 315 AA; 37973 MW; 913F5C6F0F88B316 CRC64;
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KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 315 AA; 36269 MW; CECE4DAEE54D24E4 CRC64;

Query Match
Best Local Similarity 90.1%; Score 1596; DB 11; Length 315;
Matches 293; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 14 LRHQGKPSDAGPHGQGRVHOAAPLSDAPHDDAHGQFYDHEAFLGREAFAKEDQLTLP 73
Db 1 LRHWLGKPSDAGPHGQGRVHHGTPLSSEAPDDAHGQFYDHEAFLGRDVAKEFDKLSP 60

QY 74 EESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSAAWDYTDGRGV 133
Db 61 EESQARLGRIVDRMDLAGDGGWVSLAELRAWIAHTQQRHIRDSVSAAWHYTDGRGV 120

QY 134 GWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGDGSMATREELTAF 193
Db 121 GWEELRNATYGHYEPGEEFHDVEDAETKKMLARDERRFRVADQDGDGSMATREELTAF 180

QY 194 PEEFPHMRDIVIAETLEDLRNKDGYVOVEEYIADLYSAEPGEEPAWVQTERQOQFDR 253
Db 181 PEEFPHMRDIVIAETLEDLRNKDGYVOVEEYIADLYSEEPGEEPAWVQTERQOQFDR 240

QY 254 DLNKGHLGDSGVGHVWLPAPQDQPLVEANHLHESDTRKDKRLSKAEILGNMNFVGSQ 313
Db 241 DLNKGDLGDSGVGHVWLPAPQDQPLVEANHLHESDTRKDKRLSKAEILGNMNFVGSQ 300

QY 314 ATNYGEDLTRHDEL 328
Db 301 ATNYGEDLTRHDEL 315

RESULT 5
Q9CTD4 PRELIMINARY; PRT; 259 AA.
AC Q9CTD4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 6030455P07Rik protein (Fragment).
GN 6030455P07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=EMBRYO;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombarts P.,
RA Nordone P., Ring B., Ringwald J., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003918; BAB23076.1;
DR MGD; MGI:1915346; 6030455P07Rik.
InterPro; IPR002048; EF-hand.

DR InterPro; IPR000886; ER-target.
DR Pfam; PF00036; efhand; 4.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF-HAND; UNKNOWN_4.
DR PROSITE; PS00014; ER-TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 259 AA; 30163 MW; 7910A9F0476260A1 CRC64;

Query Match
Best Local Similarity 74.5%; Score 1321; DB 11; Length 259;
Matches 244; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 70 QLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSAANDYTDTR 129
Db 1 KLTPEESQARLGRIVDRMDLAGDGGWVSLAELRAWIAHTQQRHIRDSVSAARWYTDTR 60

QY 130 DGRVGHWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGDGSMATREELT 189
Db 61 DGRVGHWEELRNATYGHYEPGEEFHDVEDAETKKMLARDERRFRVADQDGDGSMATREELT 120

QY 190 AFLHPEEFPHMRDIVIAETLEDLRNKDGYVOVEEYIADLYSAEPGEEPAWVQTERQOQF 249
Db 121 AFLHPEEFPHMRDIVIAETLEDLRNKDGYVOVEEYIADLYSEEPGEEPAWVQTERQOQF 180

QY 250 RFRDLNKGHLGDSGVGHVWLPAPQDQPLVEANHLHESDTRKDKRLSKAEILGNMNF 309
Db 181 RFRDLNKGDLGDSGVGHVWLPAPQDQPLVEANHLHESDTRKDKRLSKAEILGNMNF 240

QY 310 VGSQATNYGEDLTRHDEL 328
Db 241 VGSQATNYGEDLTRHDEL 259

RESULT 6
Q93434 PRELIMINARY; PRT; 322 AA.
AC Q93434;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Reticulocalbin.
GN RCN1.
OS Fuqu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
ON NCBI_TaxID=31033;
RP SEQUENCE FROM N.A.
RX MEDLINE=99007268; PubMed=9789042;
RA Miles C., Elgar G., Coles E., Kleinjan D.J., Van Heyningen V.,
RA Hastie N.;
RT "Complete sequencing of the Fuqu WAGR region from wt1 to pax6;
RT Dramatic compaction and conservation of synteny with human chromosome
RT 11p13."
RL Proc. Natl. Acad. Sci. U.S.A. 95:13068-13072(1998).
DR EMBL; AL021531; CAA16492.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER-target.
DR Pfam; PF00036; efhand; 6.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF-HAND; UNKNOWN_4.
DR PROSITE; PS00014; ER-TARGET; UNKNOWN_1.
SQ SEQUENCE 322 AA; 38207 MW; 85F99C053AC34C5C CRC64;

Query Match
Best Local Similarity 51.4%; Score 911; DB 13; Length 322;
Matches 167; Conservative 50; Mismatches 69; Indels 4; Gaps 3;

QY 40 LSDAPHDDAHGQFYDHEAFLGREAFAKEDQLTPEESQARLGRIVDRMDRAGDGGWVSL 99
Db 36 LQOATNED-NNSFQVDHEVFLGKESTFDQLSPESKDRLSKIVDRID--GDGNSYITT 92

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QY	100	ALRAWIAHQORHSDVSAAWDTYDTRDGRVGEELRNATYGHYAPG-EFFHVEDA	158
Db	93	DELKAWTKRVQKRYVENVVWADYDLNKNKISWEEYKATYGYLNPFEEDTDD	152
QY	159	ETVKMLARDERRFRVADQDGMATREELTAFLHPEEPHMDIVIAETLEDLDRKDG	218
Db	153	FSFKMLPRDRERFRKADLDGSAANREFTSLHPEEFHMDIVVLETLEDIDKNSDG	212
QY	219	YVQVEEYIADLYSAEPGEPAWVQTERQFRDLNKGDLGDSGVGHVWLPQAQDP	278
Db	213	HVDEYIADWFAHEDRGPPEWVKTERQFSDFRDLNKGDLGDLIRHWINPQDYDHA	272
QY	279	LVEANHLHESDTDKGRLSKAEILGNMNFVGSQATNYGEDITLRHDEL	328
Db	273	QAEARHLVYESDKDKQDLKKEILDNMNFVGSQATNYGEDITLRHDEL	322
RESULT 7			
ID	Q96RL3	PRELIMINARY; PRT; 315 AA.	
AC	Q96RL3		
DT	01-DEC-2001	(Tremblrel. 19, Created)	
DT	01-DEC-2001	(Tremblrel. 19, Last sequence update)	
DT	01-MAR-2002	(Tremblrel. 20, Last annotation update)	
DE	Calumenin.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Peterson R.E. Jr., Watson D.K.;		
RT	"Novel splice variant of human calumenin.";		
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF345637; AAK72908.1; -		
DR	InterPro; IPR002048; EF-hand.		
DR	Pfam; PF00036; ehand; 6.		
DR	PROSITE; PS00018; EF_HAND; UNKNOWN_4.		
DR	PROSITE; PS00018; EF_HAND; UNKNOWN_4.		
FT	NON_TER 1		
SQ	SEQUENCE 315 AA; 37135 MW; EIBF415B25076676 CRC64;		
Query Match	48.4%;	Score 857.5; DB 4; Length 315;	
Best Local Similarity	50.5%;	Pred. No. 2.9e-56;	
Matches	161; Conservative	62; Mismatches 85; Indels 11; Gaps 4;	
QY	8	LLLLLLRHGAQKPSDAGPHGQGRVHQAPLSDAPHDDAHGNGFYDHEAFLGREVAKE	67
Db	7	LMCLSLCTAFALSKPT-----EKKDRVHHEPOLSKVHNDQAQ-SFYDHDAPLGAEEAKT	60
QY	68	FDLTPEESQARLGRVDRMDRAGDGGVSLAELRAWIAHQORHSDVSAAWDTYDT	127
Db	61	FDLTPEESKERLGMIVDKID--ADKGFVTEGELKSWIKHAQKVIYDNVENQWQEFDM	118
QY	128	DRDGRVGEELRNATYGHYAPGEFFHVEDAETYYKKMLARDERRFRVADQDGMATRE	187
Db	119	NQDGLISDYEIRNVYTGTVL---DDPDGDFGNKYOMVYRDERFRKMDKDGDLATKEE	175
QY	188	LTAFHPEEPHMDIVIAETLEDLDRNKGQVQVEEYIADLYSAEPGEPAWVQTERQ	247
Db	176	FTAFHPEEYDMKDIVVQETMEDIDKADGFDIDLEYIGDMYSHDGNTEDEPWVKTERE	235
QY	248	QFRDRLNKGDLGDSGVGHVWLPQAQDPVLVEANHLHESDTDKGRLSKAEILGNM	307
Db	236	QFVEFRDKNKGDKMDEETKDWLPSDYDHAEAEARHLVYESDONKDKGLTKEEIVDKYD	295
QY	308	MFVGSQATNYGEDITLRHHD 326	
Db	296	LFVGSQATDFGEALVRHDE 314	
RESULT 8			
ID	Q9NR43	PRELIMINARY; PRT; 296 AA.	
QY	Q9NR43		


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DE 174 VADQDGSMTARELTAFLLHPEEFPHMRDIVIAETLEDLRNKGQVQVEEYIADLYSAE 233
GN M03F4.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OC NCBI_TaxID=6239;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RC STRAIN=BRISTOL N2;
RA Yabe D.;
RT "Caenorhabditis elegans homolog of mouse calumenin."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RC STRAIN=BRISTOL N2;
RA Fulton L.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF228528; AAF34189.1; -.
DR EMBL; U64601; AAB04578.1; -.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; eFhand; 5.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_5.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_5.
SQ SEQUENCE 314 AA; 36077 MW; 0350F2C8CDA3AA62 CRC64;

Query Match 36.1%; Score 639.5; DB 5; Length 314;
Best Local Similarity 40.0%; Pred. No. 5.6e-40;
Matches 132; Conservative 63; Mismatches 100; Indels 35; Gaps 8;

QY 7 VLLLLLLRHGA-----QGKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNGFOYDHEAFILG 61
Db 3 VLFVGLLAATALASHHSDPSKD-GEHFKGKEHDK-----KYDHEQFLG 46
QY 62 REVAKEDQLTLPESQARLGRIVDRMDRAGDGGWVSLAEALRAWTAHTOORHIRDSVNA 121
Db 47 KDTAAEFDELTPESKKEKLAFLPKMD--ADSGFTEENELKDHINFMQRYVNDVDRT 104
QY 122 WDVTDTDR--DGRVGEELRNATYGHY-APGEFHDVEDEATYKMLARDERRFRVADQD 178
Db 105 WKYKAELKIVDGKIKWEDYEMVYGSADGAGQEL-----SPEYAKMIARDEKQWAVADY 159
QY 179 GDSMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGQVQVEEYIADLYSAEPGEE- 237
Db 160 .SNGALDRTEYCGFMPECDCHMDRVVVAETVDDIDKKNKGSVDLDEYIGMYPDDYP 219
QY 238 ---EPAWQTERQOQFRDRLNKGDLGSEVGHVWLPAPADQQLVPEANHLHESDTPKD 294
Db 220 NGKEPDWQSEREMFKEHRDKDGGKLNQEEEMRDNIHPVGFDAEAEARHLVGIADNDK 279
QY 295 GLSKAEILGNMFMVGSQATNYGEDLTRH 324
Db 280 GKLNLDEIVAHYDTFVGSQATDYGEOLQKH 309

RESULT 14
ID Q63399 PRELIMINARY; PRT; 98 AA.
AC Q63399;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE (clone REMI) ORF (fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HOLZMAN; IISUE=BRIN;
RX MEDLINE=9623155; PubMed=8642059;
RA Asakura K., Pogulis R.J., Pease L.R., Rodriguez M.;
RT "A monoclonal autoantibody which promotes central nervous system
remyelination is highly polyreactive to multiple known and novel

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QY 174 VADQDGSMTARELTAFLLHPEEFPHMRDIVIAETLEDLRNKGQVQVEEYIADLYSAE 233
GN M03F4.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OC NCBI_TaxID=6239;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RC STRAIN=BRISTOL N2;
RA Yabe D.;
RT "Caenorhabditis elegans homolog of mouse calumenin."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RC STRAIN=BRISTOL N2;
RA Fulton L.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF228528; AAF34189.1; -.
DR EMBL; U64601; AAB04578.1; -.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; eFhand; 5.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_5.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_5.
SQ SEQUENCE 314 AA; 36077 MW; 0350F2C8CDA3AA62 CRC64;

Query Match 36.1%; Score 639.5; DB 5; Length 314;
Best Local Similarity 40.0%; Pred. No. 5.6e-40;
Matches 132; Conservative 63; Mismatches 100; Indels 35; Gaps 8;

QY 7 VLLLLLLRHGA-----QGKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNGFOYDHEAFILG 61
Db 3 VLFVGLLAATALASHHSDPSKD-GEHFKGKEHDK-----KYDHEQFLG 46
QY 62 REVAKEDQLTLPESQARLGRIVDRMDRAGDGGWVSLAEALRAWTAHTOORHIRDSVNA 121
Db 47 KDTAAEFDELTPESKKEKLAFLPKMD--ADSGFTEENELKDHINFMQRYVNDVDRT 104
QY 122 WDVTDTDR--DGRVGEELRNATYGHY-APGEFHDVEDEATYKMLARDERRFRVADQD 178
Db 105 WKYKAELKIVDGKIKWEDYEMVYGSADGAGQEL-----SPEYAKMIARDEKQWAVADY 159
QY 179 GDSMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGQVQVEEYIADLYSAEPGEE- 237
Db 160 .SNGALDRTEYCGFMPECDCHMDRVVVAETVDDIDKKNKGSVDLDEYIGMYPDDYP 219
QY 238 ---EPAWQTERQOQFRDRLNKGDLGSEVGHVWLPAPADQQLVPEANHLHESDTPKD 294
Db 220 NGKEPDWQSEREMFKEHRDKDGGKLNQEEEMRDNIHPVGFDAEAEARHLVGIADNDK 279
QY 295 GLSKAEILGNMFMVGSQATNYGEDLTRH 324
Db 280 GKLNLDEIVAHYDTFVGSQATDYGEOLQKH 309

RESULT 14
ID Q63399 PRELIMINARY; PRT; 98 AA.
AC Q63399;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE (clone REMI) ORF (fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HOLZMAN; IISUE=BRIN;
RX MEDLINE=9623155; PubMed=8642059;
RA Asakura K., Pogulis R.J., Pease L.R., Rodriguez M.;
RT "A monoclonal autoantibody which promotes central nervous system
remyelination is highly polyreactive to multiple known and novel

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RT antigens.*;
RL J. Neuroimmunol. 65:11-19(1996).
DR EMBL: L41683; AAB05841.1; -.
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; ehand; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
FT NON_TER 1
FT TER 98
SQ SEQUENCE 98 AA; 11277 MW; FOA3D6D9EF624CE1 CRC64;

Query Match 27.1%; Score 481; DB 11; Length 98;
Best Local Similarity 93.7%; Pred. No. 7.7e-29;
Matches 89; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 62 REVAKFQDQTPESQARLGRIVDRMDRAGDGGWLSLAELRAWTAAHQOIRHDSVSA 121
Db 2 RDKAKFQDQTPESQARLGRIVDRMDRAGDGGWLSLAELRAWTAAHQOIRHDSVSA 61

QY 122 WDYTDTRDGRVGEELRNATYCHYAPGEEFHDE 156
Db 1 RDKAKFQDQTPESQARLGRIVDRMDRAGDGGWLSLAELRAWTAAHQOIRHDSVSA 61

QY 62 WDYTDTRDGRVGEELRNATYCHYAPGEEFHDE 96
Db 1 RDKAKFQDQTPESQARLGRIVDRMDRAGDGGWLSLAELRAWTAAHQOIRHDSVSA 61

RESULT 15
Q9VMV2 PRELIMINARY; PRT: 342 AA.
AC Q9VMV2;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE CG9112 protein (LD34388P).
GN CG9112.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_taxid=7227;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flesler C., Gabriellista A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glisak A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimori I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnik S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: A8003608; AAF52207.1; -.
DR EMBL: AY061412; AAL28960.1; -.
DR HSSP: P02593; 1CDM.
DR FlyBase: FBgn0031673; CG9112.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00036; ehand; 6.
DR SMART: SM00054; Efh; 3.
DR PROSITE: PS00018; EF_HAND; 4.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
KW Calcium-binding.
SQ SEQUENCE 342 AA; 39453 MW; C3C0D0F75ADC8286 CRC64;

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Query Match 25.8%; Score 457; DB 5; Length 342;
Best Local Similarity 33.7%; Pred. No. 2.7e-26;
Matches 118; Conservative 59; Mismatches 131; Indels 42; Gaps 13;

QY 5 PSVLLLLLRHGAQKPSDAGPHGQGRVHQA-----APLSDAPH--DDAAG 50
Db 9 PLTICAVALL---AAVGMPAHGAVANSHKHEKLSKRVKDGTYAP-RDAHHHGEGEH 64

QY 51 NFQYDHEAFGR-EVAKFQDQTPESQARLGRIVDRMDRAGDGGWLSLAELRAWTAAHT 109
Db 65 NYEFDHEAIIQNTKEAQEFDSLSPDESKRRLLILIKMMDL--NKDEFIDRHLKAWLRS 122

QY 110 QQRHSDSVSAWDYTDTRDGRVGEELRNATYCHYAPGEEH----DVEDAETKKML 165
Db 123 FKKLSEEAADRFEIDQDADERITWKEYLQDTYA--MEDEFKKETIDYDSYDEQKMI 180

QY 166 ARDERFRVADQDGDGMATREELTAFLHPBEFPHMRDIVIAETLEDRNKGQYVOVEEY 225
Db 181 KQDKEMNAADTNKDGVLTLTEEFVLFQNPBEHPQMLPILLEHTMQDKADHDGKINQFQ 240

QY 226 IADLYSAEPGEEEPANVQTERQDFRDLNKGHLGDSGVGHVLP-----AQDQPLVE 281
Db 241 VGDAAS----HDKEWLITKEKFDKDHDSNGDGVLTGDEVLSWIYPSNTAAND----E 292

QY 282 ANHLHSDTDKGRLSKABILGNMNFVGSQATNYGDELTR--HH--DEL 328
Db 293 VDHLFVSTDHDDRLSYLEILNNYTFVGSSEATDYGDLHQLNHLNLSDEL 342

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Search completed: May 14, 2003, 10:45:29
Job time : 107.883 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:34:22 ; Search time 27.8944 Seconds
 (without alignments)
 487.704 Million cell updates/sec

Title: US-09-768-840-1
 Perfect score: 1772
 Sequence: 1 MMWRPSVLLLLLLRHGAG.....FVGSQATNYGEDLIRHDEL 328

Scoring table:
 BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	944	53.3	331	1	RCN1_HUMAN
2	938	52.9	325	1	RCN1_MOUSE
3	845.5	47.7	315	1	CALU_MOUSE
4	842.5	47.5	315	1	CALU_HUMAN
5	476	26.9	318	1	RCN2_RAT
6	456.5	25.8	317	1	RCN2_HUMAN
7	269.5	15.2	362	1	CB45_HUMAN
8	261.5	14.8	361	1	CB45_MOUSE
9	260.5	14.7	361	1	CB45_MOUSE
10	138.5	7.8	344	1	TCB3_ARATH
11	134.5	7.6	169	1	CAF1_DICDI
12	134.5	7.6	276	1	SEG1_HUMAN
13	129.5	7.3	275	1	CAB4_HUMAN
14	129	7.3	321	1	LPSA_LYPTI
15	128	7.2	134	1	CABP_ENTHI
16	127.5	7.2	271	1	CLB2_MOUSE
17	127	7.2	271	1	CLB2_MOUSE
18	127	7.2	271	1	CLB2_MOUSE
19	126.5	7.1	215	1	CAB2_MOUSE
20	126	7.1	269	1	CLB2_CHICK
21	125.5	7.1	243	1	LPSB_LYPTI
22	124.5	7.0	148	1	CLM4_MOUSE
23	124.5	7.0	160	1	TPCS_ANGAN
24	124	7.0	146	1	CLSP_HUMAN
25	123	6.9	162	1	CAB2_BOVIN
26	119.5	6.7	513	1	CDP2_MAIZE
27	118.5	6.7	162	1	TPCS_MELGA
28	118.5	6.7	219	1	CAB2_HUMAN
29	118	6.7	533	1	CDP2_ORYSA
30	117.5	6.6	143	1	SM16_SCHMA
31	117.5	6.6	162	1	TPCS_RANES
32	116.5	6.6	610	1	CDP1_ARATH
33	115.5	6.5	162	1	TPCS_CHICK

34 114.5 6.5 150 1 SP15_HEMPU
 35 114.5 6.5 175 1 CALC_RAT
 36 114.5 6.5 189 1 NCS1_YEAST
 37 113 6.4 149 1 CABO_LOLPE
 38 112.5 6.3 178 1 CALC_MOUSE
 39 112 6.3 165 1 POC2_JUNOX
 40 111 6.3 152 1 SPIA_STRPU
 41 111 6.3 163 1 TPC_BRALA
 42 111 6.3 176 1 CATR_GIALA
 43 110 6.2 149 1 CALM_WHEAT
 44 109.5 6.2 148 1 CALM_METSE
 45 109.5 6.2 148 1 CALM_PATSP

ALIGNMENTS

RESULT 1

RCN1_HUMAN STANDARD; PRT; 331 AA.

ID RCN1_HUMAN
 AC Q15293;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Reticulocalbin 1 precursor.
 GN RCN1 OR RCN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96172582; PubMed=8586628;
 RA Ozawa M.;
 RT "Cloning of a human homologue of mouse reticulocalbin reveals
 conservation of structural domains in the novel endoplasmic reticulum
 resident Ca(2+)-binding protein with multiple EF-hand motifs.";
 RL J. Biochem. 117:1113-1119(1995).
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Coville G.;
 RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: MAY REGULATE CALCIUM-DEPENDENT ACTIVITIES IN THE
 CC ENDOPLASMIC RETICULUM LUMEN OR POST-ER COMPARTMENT.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 CC SITES; POTENTIAL SITES II AND VI HAVE LOST AFFINITY FOR CALCIUM
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CREC FAMILY.
 CC -1- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC -----
 CC EMBL; D42073; BAA07670.1; -
 CC EMBL; AL078612; CAB53067.1; -
 CC Genem; HGNC:9934; RCN1.
 CC MIM; 602735; -
 CC InterPro; IPR002048; EF-hand.
 CC InterPro; IPR000886; EF_target.
 CC Pfam; PF00036; ehand; 6.
 CC SMART; SM00034; EFh; 3.
 CC PROSITE; PS00014; ER_TARGET; 1.
 CC PROSITE; PS00018; EF_HAND; 4.
 CC Calcium-binding; Endoplasmic reticulum; Signal; Glycoprotein; Repeat;
 KW Polymorphism.
 FT SIGNAL 1 29
 FT CHAIN 30 331
 FT RETICULOCALBIN 1.

[illegible]

OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=93107083; PubMed=8416973;	
RA	Ozawa M., Muramatsu T.;	
RT	"Reticulocalbin, a novel endoplasmic reticulum resident	
RT	Ca(2+)-binding protein with multiple EF-hand motifs and a	
RT	carboxyl-terminal HDEL sequence.";	
RL	J. Biol. Chem. 268:699-705(1993).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RP	STRAIN=129/SV; TISSUE=Liver;	
RX	MEDLINE=96015163; PubMed=8537305;	
RC		


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QY 181 SMATREELTAFLHPPEPHMRDVIATLEDLDRNKDGYVOVEYIADLYSABPGEPEA 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 178 LTATREELTAFLHPPEPHMRDVIATLEDLDRNKDGYVOVEYIADLYSABPGEPEA 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 WYOTERQOFRDLNKGDLGSEVGHVLPAPQDPLVEANHLHESDTRKDGRLSKA 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 238 WYLSERQOFRDLNKGDLGSEVGHVLPAPQDPLVEANHLHESDTRKDGRLSKA 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 EILGNWNVFSGQATNGEDLTRHDEL 328
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 298 EILGNWNVFSGQATNGEDLTRHDEL 325

RESULT 3
CALU_MOUSE STANDARD; PRT; 315 AA.
AC O35887;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calumenin precursor.
GN CALU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10990;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=ICR; TISSUE=Heart;
RX MEDLINE=97364750; PubMed=9218460;
RA Yabe D., Nakamura T., Kanazawa N., Tashiro K., Honjo T.;
RT "Calumenin, a Ca2+-binding protein retained in the endoplasmic
RL reticulum with a novel carboxyl-terminal sequence, HDEF.";
RL J. Biol. Chem. 272:18232-18239(1997).
CC -!- FUNCTION: NOT KNOWN, BINDS 7 CALCIUM IONS WITH A LOW AFFINITY (BY
CC similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: BELONGS TO THE CREC FAMILY.
CC -!- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL: U81829; AAC3316.1; -.
GDB: MGI:1097158; Calu.
InterPro: IPR02048; EF-hand.
Pfam: PF00036; ehand; 6.
SMART: SM00054; EFh; 2.
DR PROSITE: PS00018; EF_HAND; 4.
KW Calcium-binding; Endoplasmic reticulum; Signal; Repeat.
FT SIGNAL 1 19
FT CHAIN 20 315
FT CA_BIND 81 92
FT CA_BIND 117 128
FT CA_BIND 164 175
FT CA_BIND 201 212
FT CA_BIND 242 253
FT CA_BIND 278 289
FT CARBOHYD 131 131
FT SITE 312 315
FT SEQUENCE 315 AA; 37063 MW; 742361814171E273 CRC64;
Query Match 47.78; Score 845.5; DB 1; Length 315;
Best Local Similarity 50.58; Pred. No. 4.3e-52;
Matches 161; Conservative 59; Mismatches 88; Indels 11; Gaps 4;
QY 8 LLLLLLHRAAGKSPDAGPHGQGRVHQAPLSDAPHDHAGNFQVDHEAFLGREVAKE 67.

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Db 7 LKLSLCTAFALSAPT-----EKKDRVHHPQLSDKVHNDQA-NFYDHDHDAFLGAEAKS 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 68 FDQLTPESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTOORHRSVSAAWDYDT 127
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 FDQLTPESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTOORHRSVSAAWDYDT 127
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 128 DRGRVQWEEURNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQDGSNATREE 187
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 119 NEDGLVSWEYKNTATGYVL---DDPPDDGPNYKMMYRDERFRFMAKDKGLATREE 175
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 188 LTAFLEHPEEPHMRDVIATLEDLDRNKDGYVOVEYIADLYSABPGEPEAWQTERQ 247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 176 FTAFLEHPEEYDKMDIVVQETMEDIDKNAGFDLDEEYIGDMYSHDGNADPEWKTRE 235
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 248 QFRDRLNKGDLGSEVGHVLPAPQDPLVEANHLHESDTRKDGRLSKAELGNWN 307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 236 QFYEFDRDKNRDGMKDEETKDWILPSDYDHAERAEARHLVYESDQNKDKGLKEEIVDKYD 295
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 308 MFVGSQATNGEDLTRHHD 326
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 296 LFVGSQATNGEDLTRHHD 314
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
CALU_HUMAN STANDARD; PRT; 315 AA.
AC O43852; OS0456;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calumenin precursor (IEF SSP 9302).
GN CALU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CALCIUM-BINDING DATA.
RC TISSUE=Keratinocytes;
RX PubMed=9675259;
RA Vorum H., Liu X., Madsen P., Rasmussen H.H., Honore B.;
RT "Molecular cloning of a cDNA encoding human calumenin, expression in
RL Escherichia coli and analysis of its Ca2+-binding activity.";
RL Biochim. Biophys. Acta 1386:121-131(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98260687; PubMed=9598325;
RA Yabe D., Tanigaki M., Nakamura T., Kanazawa N., Tashiro K., Honjo T.;
RT "Human calumenin gene (CALU): cDNA isolation and chromosomal mapping
RN to 7q32.";
RN Genomics 49:331-333(1998).
RP SUBCELLULAR LOCATION.
RX PubMed=10222138;
RA Vorum H., Hager H., Christensen B.M., Nielsen S., Honore B.;
RT "Human calumenin localizes to the secretory pathway and is secreted to
RL the medium.";
RL Exp. Cell Res. 248:473-481(1999).
CC -!- FUNCTION: NOT KNOWN, BINDS 7 CALCIUM IONS WITH A LOW AFFINITY.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen and secreted.
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed. Expressed at high
CC levels in heart, placenta and skeletal muscle, at lower levels in
CC lung, kidney and pancreas and at very low levels in brain and
CC liver.
CC -!- SIMILARITY: BELONGS TO THE CREC FAMILY.
CC -!- SIMILARITY: CONTAINS 7 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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```


OC Eukaryota; Metazoa; Chordata; Mammalia; Muridae; Murinae; Rattus.
CC Mammalia; Eutheria; Rodentia; Sciurognathi;
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=95239201; PubMed=7722520;

FT	CARBOHYD	40	40	N-TERMINAL (GLCNAC...)
FT	CONFLICT	70	78	DGHLNRGFH -> ERALKSGFQ (IN REF. 2).
FT	CONFLICT	86	97	DUGGEDAEPR -> NVALIGNGAP (IN REF. 2).
FT	CONFLICT	150	150	D -> G (IN REF. 2).
FT	CONFLICT	281	282	DR -> KK (IN REF. 2).
FT	CONFLICT	286	286	F -> L (IN REF. 2).
FT	CONFLICT	322	325	MIAV -> IRL (IN REF. 2).
FT	CONFLICT	356	356	R -> S (IN REF. 2).
FT	SEQUENCE	362 AA;	41807 MW;	440C6990149AAE2C CRC64;
Query Match		15.2%	Score 269.5;	DB 1; Length 362;
Best Local Similarity		25.1%	Pred. No. 6.3e-12;	
Matches		75; Conservative	63; Mismatches 136;	Indels 25; Gaps 8;
QY	47 DAHGNFQDHEAFLGREVAKEFFDLTPESQARLGRIVDMRAGDGWVSLAELRAWI	106		
Db	70 DGHLNRPFOHEVLKGLGGDEDAEPKRKRKLWVFISKVD--VNTDRKISAKEMQRWI	127		
QY	107 AHTQQRHIDRSYA--WDVTDTDRCGRVGEELR---NATYGHYAPGEFHVV----	155		
Db	128 MEKTABHFQEAWESEKTHFRAYDPDGDGVHSWDEYKVYKFLASKGH--SEKEVADAIRLNE	185		
QY	156 ---EDAEITYKKMLARDERRFRVADOGDSMATRELTAFLLHPPEFPHMRDIVIAETLEDL	212		
Db	186 ELKVDTEQTVLENLKDWRVQADSPADLLTTEEFUSFLPERSRGMLRFMYKEIVROL	245		
QY	213 DRNKDGYVQVEEVIA--DLYSAPGEE--EPAVQTERTQQRDFRDLNKGCHLDGSVGHH	268		
Db	246 DQDGDKOLSPFEFLIPVGTVENQQODIDNNWKDKRKKFEELIDNSHDGIVTAEELES	305		
QY	269 WLPVPADQQLVEANHLHSHDDKGRLSKAELIGNWNMFVGSQATNYGBDLTRHDE	327		
Db	306 YMDPMNEYNALNEAKOMIAVADENQHHLPEPELVLYSEFTFGSKLVDYARSV---HEE	361		
RESULT 8				
ID	CB45_RAT	STANDARD;	PRT;	361 AA.
AC	Q91ZS3;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	45 kDa calcium-binding protein precursor (Cab45) (stromal cell-derived factor 4) (SF-4).			
DE	SDF4 OR CAB45.			
GN	Rattus norvegicus (Rat).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxId=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BDIX;			
RA	Zhu Y., Wang M., Lin H., Luo J.;			
RT	"A calcium binding protein Cab45, identified in rat and up-regulated after alcohol."			
RL	Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: MAY REGULATE CALCIUM-DEPENDENT ACTIVITIES IN THE ENDOPLASMIC RETICULUM LUMEN OR POST-ER COMPARTMENT.			
CC	-1- SUBCELLULAR LOCATION: Golgi lumen (by similarity).			
CC	-1- SIMILARITY: BELONGS TO THE CREC FAMILY.			
CC	-1- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; AF405545; ALA01370.1; --			
DR	InterPro; IPRO02048; EF-hand.			

FT	CA_BIND	142	153	EF-HAND 4 (POTENTIAL)
SQ	SEQUENCE	169 AA;	19487 MW;	34D7D3278A569187 CRC64;
FT	CONFLICT	71	72	CV -> NL (IN REF. 3).
FT	CONFLICT	223	226	QTRA -> KOKL (IN REF. 1).
SQ	SEQUENCE	324 AA;	36807 MW;	94277BFC2D2C5CE CRC64;
	Query Match	7.8%;	Score 138.5;	DB 1; Length 324;
	Best Local Similarity	20.5%;	Pred. No. 0.0073;	Indels 69; Gaps 10;
	Matches	56; Conservative	51; Mismatches	97;
QY	69	DQLTPESQARLGRIVDRMDRAGDGGWGSUAEUAWIAHQHHRDVSAAWDYDID	128	
DB	8	DQITEYRESFRL	59	
QY	129	RGRVWEEL	175	
DB	60	GDGTIDFPEFLCVMARN	109	
QY	176	DQDGDGMATREELTAFLHPPEPHMRDIV	224	
DB	110	DKNKGDSITKEL	157	
QY	225	YIADLYSAEPGEPEPAWQTE	270	
DB	158	FLYLMAKNOGHQAPRHKTWYDQDQLEPREFRVF-DKNGDGYITVNELTMM	216	
QY	271	LPPAQDQPLVEANHLHESDTRDKDGRLSKAEIL	303	
DB	217	RLSGTQTKAELQDMINEADADGDGTISFSEV	249	
RESULT 11	CAFL_DICDI	STANDARD;	PRT;	169 AA.
AC	P54670;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Calumirin-1.			
GN	CAFA OR CAF-1.			
OS	Dictyostelium discoideum (Slime mold).			
OC	Eukaryota; Eukaryota; Dictyostelid; Dictyostelium.			
OX	NCBI_TaxID=44689;			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=AX2;			
RA	Abe F., Maeda Y.;			
RT	"Specific expression of a gene encoding a novel calcium-binding			
RT	protein, CAF-1, during transition of Dictyostelium cells from growth			
RT	to differentiation."			
RL	Dev. Growth Differ. 37:39-48(1995).			
CC	-!- FUNCTION: MAY BE INVOLVED IN THE PHASE-SHIFT OF CELLS FROM GROWTH			
CC	TO DIFFERENTIATION.			
CC	-!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN CELLS STARVED JUST			
CC	BEFORE THE PUTATIVE SHIFT POINT.			
CC	-!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; D29986; BAA06266.1;			
DR	DictyDb; DD00006; cafa.			
DR	InterPro; IPR002048; EF-hand.			
DR	PFAM; PF00036; ehand; 4.			
DR	SMART; SM00054; EFh; 2.			
DR	PROSITE; PS00018; EF_HAND; 2.			
KW	Calcium-binding; Repeat.			
FT	CA_BIND	19	30	EF-HAND 1 (POTENTIAL).
FT	CA_BIND	55	66	EF-HAND 2 (POTENTIAL).
FT	CA_BIND	106	117	EF-HAND 3 (POTENTIAL).

FT	CA_BIND	142	153	EF-HAND 4 (POTENTIAL)
SQ	SEQUENCE	169 AA;	19487 MW;	34D7D3278A569187 CRC64;
FT	CONFLICT	71	72	CV -> NL (IN REF. 3).
FT	CONFLICT	223	226	QTRA -> KOKL (IN REF. 1).
SQ	SEQUENCE	324 AA;	36807 MW;	94277BFC2D2C5CE CRC64;
	Query Match	7.8%;	Score 138.5;	DB 1; Length 324;
	Best Local Similarity	20.5%;	Pred. No. 0.0073;	Indels 69; Gaps 10;
	Matches	56; Conservative	51; Mismatches	97;
QY	69	DQLTPESQARLGRIVDRMDRAGDGGWGSUAEUAWIAHQHHRDVSAAWDYDID	128	
DB	8	DQITEYRESFRL	59	
QY	129	RGRVWEEL	175	
DB	60	GDGTIDFPEFLCVMARN	109	
QY	176	DQDGDGMATREELTAFLHPPEPHMRDIV	224	
DB	110	DKNKGDSITKEL	157	
QY	225	YIADLYSAEPGEPEPAWQTE	270	
DB	158	FLYLMAKNOGHQAPRHRTKTKTWYDQLDDQILEPREFRVF-DKNGDGYITVNELRTM	216	
QY	271	LPPAQDQPLVEANHLHESDTRDKDGRLSKAEIL	303	
DB	217	RLSGETQTKAELQDMINEADADGDGTISFSEV	249	
RESULT 11	CAFL_DICDI	STANDARD;	PRT;	169 AA.
AC	P54670;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Calumirin-1.			
GN	CAFA OR CAF-1.			
OS	Dictyostelium discoideum (Slime mold).			
OC	Eukaryota; Eukaryota; Dictyostelid; Dictyostelium.			
OX	NCBI_TaxID=44689;			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=AX2;			
RA	Abe F., Maeda Y.;			
RT	"Specific expression of a gene encoding a novel calcium-binding			
RT	protein, CAF-1, during transition of Dictyostelium cells from growth			
RT	to differentiation."			
RL	Dev. Growth Differ. 37:39-48(1995).			
CC	-!- FUNCTION: MAY BE INVOLVED IN THE PHASE-SHIFT OF CELLS FROM GROWTH			
CC	TO DIFFERENTIATION.			
CC	-!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN CELLS STARVED JUST			
CC	BEFORE THE PUTATIVE SHIFT POINT.			
CC	-!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; D29986; BAA06266.1;			
DR	DictyDb; DD00006; cafa.			
DR	InterPro; IPR002048; EF-hand.			
DR	PFAM; PF00036; ehand; 4.			
DR	SMART; SM00054; EFh; 2.			
DR	PROSITE; PS00018; EF_HAND; 2.			
KW	Calcium-binding; Repeat.			
FT	CA_BIND	19	30	EF-HAND 1 (POTENTIAL).
FT	CA_BIND	55	66	EF-HAND 2 (POTENTIAL).
FT	CA_BIND	106	117	EF-HAND 3 (POTENTIAL).


```

-|- FUNCTION: CALCIUM-BINDING PROTEIN INVOLVED IN LARVAL DEVELOPMENT
AND METAMORPHOSIS. LIKELY TO FUNCTION AS CALCIUM BUFFERS
MEDIATING THE TRANSPORT OF CALCIUM FROM THE SEA WATER TO THE
BLASTOCOELE WHERE CALCIUM IS REQUIRED FOR SKELETON FORMATION.
-|- TISSUE SPECIFICITY: ABORAL ECTODERM, A SQUAMOUS EPITHELIUM
COVERING THE SURFACE OF THE LATE STAGE EMBRYO AND LARVA.
-|- DEVELOPMENTAL STAGE: ACTIVATED EARLY IN DEVELOPMENT IN ABORAL
ECTODERM CELLS.
-|- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
MORE SPECIFICALLY TO SPECS.
-----
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or send an email to license@isb-sib.ch).
-----
EMBL; J04068; AAA30007.1; ALT_INIT.
PIR; A31797; A31797.
HSP; P02593; LFW4.
InterPro; IPR002048; EF-hand.
Pfam; PF00036; ehand; 7.
ProDom; PD000012; EF-hand; 4.
SMART; SM00054; EFh; 6.
PROSITE; PS00018; EF_HAND; 7.
Calcium-binding: Repeat.
REPEAT 1 150
FT REPEAT 151 298
FT CA_BIND 29 40 EF-HAND 1.
FT CA_BIND 60 71 EF-HAND 2.
FT CA_BIND 98 109 EF-HAND 3.
FT CA_BIND 134 145 EF-HAND 4.
FT CA_BIND 178 189 EF-HAND 5.
FT CA_BIND 213 224 EF-HAND 6.
FT CA_BIND 245 256 EF-HAND 7.
FT CA_BIND 282 293 EF-HAND 8.
SEQUENCE 321 AA; 37196 MW; E6ELCAE0E3D1D88D CRC64;

Query Match 7.3%; Score 129; DB 1; Length 321;
Best Local Similarity 25.0%; Pred. No. 0.033; Indels 38; Gaps 9;
Matches 51; Conservative 40; Mismatches -----GHYAPGEEFHVEDAETKKM 164
QY 123 DTYDDRDGRGVWEB---LRNATY-----GNYDKGTVSCALVLMKNWTEMAQNIIARLDVNSDGH-MQDFEFLYMEGSTKERL 84
DB 26 DNYDKGTVSCALVLMKNWTEMAQNIIARLDVNSDGH-MQDFEFLYMEGSTKERL 84
QY 165 LARDE--RRFRVADGGDSMATRELTAFLHPPEFPHMRDIVIAETLEDLNKDGYYQV 222
DB 85 YSSDEIKOMFDLLDRGDNGRISPDELNKGV-R-EITKVVDGANKLIQEAADKGDHVM 143
QY 223 EYVIADLYSAEP-----GEEPAWVQTROEQDFRDLNKLGDGSEGVHWVLPPAQ 275
DB 144 EFFDTLVVKLPIGMCPCKDEEVREYKNEFKF----DKNGDGLSLTAAEMSEFMKSSTK 199
QY 276 --DQPLVEANHLHESDTHDKGRL 297
DB 200 YSDK---EIEYLIRVDLNDGVR 220
-----
RESULT 15
CABP_ENTHI STANDARD; PRT; 134 AA.
AC CABP_ENTHI
AC P38505;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-binding protein (CABP).
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN 11
```

search completed: May 14, 2003, 10:43:33
job time : 30.8944 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:40:47 ; Search time 50.9795 Seconds
(without alignments)
618.525 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 1772
Sequence: 1 MMWRPSVLLLLLRHGAQG.....FVGSQATNGEDLTRHDEL 328

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-73:*
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	944	53.3	331	JC4173	reticulocalbin pre
2	938	52.9	325	A45337	reticulocalbin pre
3	692	39.1	322	A57516	DNA supercoiling f
4	639.5	36.1	314	T25842	hypothetical prote
5	476	26.9	318	I56519	talpoxin-associate
6	466.5	26.3	319	JCS402	vitamin D receptor
7	456.5	25.8	317	I37371	ER calcium-binding
8	357	20.1	313	T33849	hypothetical prote
9	214.5	12.1	345	T09018	probable calcium-b
10	188	10.6	374	A42264	membrane-associate
11	175	9.9	320	T15849	hypothetical prote
12	145	8.2	571	T00835	calcium-dependent
13	138.5	7.8	324	T02109	calmodulin-like pr
14	130	7.3	521	T02109	calcium-dependent
15	129	7.3	317	A31797	Spec-related prote
16	127.5	7.2	271	A0253	calretinin - human
17	127	7.2	271	A0253	calretinin - rat
18	126.5	7.1	243	A40394	spec-related prote
19	126	7.1	269	A27067	calretinin - chick
20	124	7.0	154	T02109	calcium binding pr
21	123.5	7.0	166	T07949	probable calmoduli
22	122.5	6.9	163	TJW062	fast skeletal trop
23	122.5	6.9	536	T05500	calcium-dependent
24	121.5	6.9	544	T05500	probable calmoduli
25	120	6.8	167	TJW065	fast skeletal trop
26	119.5	6.7	163	TJW063	fast skeletal trop
27	119.5	6.7	513	T02259	calcium-dependent
28	118.5	6.7	162	A40803	troponin C, skelet
29	118.5	6.7	531	T02993	calcium-dependent

30.	118	6.7	151	2	A71409	calmodulin 8 limpo
31	118	6.7	533	1	S56652	calcium-dependent
32	117.5	6.6	162	1	TPFGCS	troponin C, skelet
33	116.5	6.6	484	2	T05650	calcium-dependent
34	116.5	6.6	610	1	A49082	calcium-dependent
35	116	6.5	582	2	E84721	probable calcium-d
36	115.5	6.5	163	1	TPCHCS	troponin C, skelet
37	114.5	6.5	150	2	JS0024	15K calcium-bindin
38	114.5	6.5	176	2	JQ1232	calcineurin regula
39	114.5	6.5	190	2	S61168	hypothetical prote
40	113.5	6.4	166	2	A86447	hypothetical prote
41	113	6.4	149	2	A33353	calcium-binding pr
42	113	6.4	150	2	H85194	hypothetical prote
43	113	6.4	246	2	T05308	hypothetical prote
44	113	6.4	246	2	H85387	hypothetical prote
45	113	6.4	540	1	T01989	calcium-dependent

ALIGNMENTS

RESULT 1

JC4173

reticulocalbin precursor - human

C:Species: Homo sapiens (man)

C>Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 02-Aug-2002

C:Accession: JC4173

R:Ozawa, M.

J. Biochem. 117, 1113-1119, 1995

A:Title: Cloning of a human homologue of mouse reticulocalbin reveals conservation of

A:Reference number: JC4173; MUID:96172582; PMID:8586628

A:Accession: JC4173

A:Molecule type: mRNA

A:Residues: 1-331 <OZA>

A:Cross-references: DDBJ:D42073; MID:g1262328; PIDN:BAA07670.1; PID:d1008252; PID:g1262328; This protein is a luminal protein of the endoplasmic reticulum, and is a c
a signal for its retention in the endoplasmic reticulum of cells.

C:Genetics:

A:Gene: GDB:RCN: Rcal

A:Cross-references: GDB:6383031

A:Map position: lpl3-11p13

C:Superfamily: reticulocalbin; calmodulin repeat homology

F:1-29/Domain: signal binding; calmodulin binding; EF hand; endoplasmic reticulum

F:30-331/Product: reticulocalbin homolog #status predicted <SIG>

F:79-111/Domain: calmodulin repeat homology #status predicted <MAT>

F:113-145/Domain: calmodulin repeat homology <EF1>

F:166-198/Domain: calmodulin repeat homology <EF2>

F:203-235/Domain: calmodulin repeat homology <EF3>

F:244-276/Domain: calmodulin repeat homology <EF4>

F:280-312/Domain: calmodulin repeat homology <EF5>

F:328-331/Region: endoplasmic reticulum retention signal

Query Match 53.3%; Score 944; DB 2; Length 331;

Best Local Similarity 54.7%; Pred. No. 1e-59; Matches 181; Conservative 51; Mismatches 75; Indels 24; Gaps 5;

QY 7 VLLLLLLRHGAQGRPS-----PDAGPHGQGRVHQAPLSDAPHDHAGNFOYDHEA 58

Db 16 LLLALLAPRVLRKPTVKRWVRPD-----SELGERPPD-NQSFQYDHEA 62

QY 59 FLGFEVAKFEEDOLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWTAHTQQRHDSV 118

Db 63 FLGKEDSKTFDQLTPEESKERLGRIVDRID--NDGDGFTTEELKTKWIKRVKRYIFDNV 120

QY 119 SAAWDTYDTRDGRVGEWELRNATYGYHAPG--EEFHDVEDAEYTKMLARDERFRVADQ 177

Db 121 AKWMDYDRDKDKISWEYKQATYGYLGNPAEFHSDSHHTFKMLPDRERFKAADL 180

QY 178 DGDSNATREELTAFLLPHEFFHMDIVTAETPLDLDRNKDGYVQVEEYIADLYSAEPGEE 237

Db 181 NGDLTATREEFATFLPHEFFHMKIEIVVLETLEDIKNGDGFVDODDYIADMF SHEENGP 240

QY 238 EPANVOTERQQRFRDLNKGHLDSGVGHVWVLPADOPPLVEANHLIHESDITDKDGR 297
 Db 241 EPDWVLSERQENFRDLNKGKLDKDEIRHWILFQDYDHAQAEARHLVYESDKNKDEKL 300

QY 298 SRAEILGNMNFVGSQATNYGEDLTRHDEL 328
 Db 301 TREIILENNMFVGSQATNYGEDLTRHDEL 331

RESULT 2
 A45337
 reticulocalbin precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002
 C:Accession: A45337; I55203
 R;Ozawa, M.; Muramatsu, T.
 J. Biol. Chem. 268, 699-705, 1993
 A:Title: Reticulocalbin, a novel endoplasmic reticulum resident Ca(2+)-binding protein
 A:Reference number: A45337; MUID:93107083; PMID:8416973
 A:Contents: teratocarcinoma OTT6050
 A:Accession: A45337
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-325 <OZA>
 A:Cross-references: GB:D13003; NID:g220581; PIDN:BAA02366.1; PID:d1002865; PID:g220582
 A:Note: sequence extracted from NCBI backbone (NCBIP:121512)
 R;Ozawa, M.
 J. Biochem. 118, 154-160, 1995
 A:Title: Structure of the gene encoding mouse reticulocalbin, a novel endoplasmic reticulum
 A:Reference number: I55203; MUID:96015163; PMID:8537305
 A:Accession: I55203
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-325 <GB>
 A:Cross-references: GB:D43956; NID:g2190295; PIDN:BAA07896.1; PID:g968894
 C:Genetics:
 A:Introns: 79/2; 144/1; 203/3; 224/1; 290/3
 C:Superfamily: reticulocalbin; calmodulin repeat homology
 C:Keywords: EF hand
 F:1-23/Domain: signal
 F:322-325/Region: endoplasmic reticulum retention signal

Query Match 52.9%; Score 938; DB 2; Length 325;
 Best Local Similarity 55.2%; Pred No. 2, 7e-59;
 Matches 181; Conservative 47; Mismatches 76; Indels 24; Gaps 5;

QY 10 LLLLLRHGAGKPS-----PDAGPHGQGRVHQAAPLSDAPHDHAGNFOYDHEAF 61
 Db 13 LLLALVALRAKPTVKRWVRPD-----SELGERPPED-NOSFOYDHEAF 59

QY 62 REVAFKFDQLTPEESQARGLRIVDRMDRAGDGDGWSYLAELRAWIAHTQOIRHRSVSA 121
 Db 60 KEDSKTFDQSPDSKERLGIKIVRID--SDGDLVTEELKWLKRVQKRYIDNVAKV 117

QY 122 WDITYDTRDRGRVGEELRNATYGHYAGP-EEFHVDVDAETKYLARDERRFVADODGD 180
 Db 118 WKDYDRDKDEKISWEYEQATYGYLGNPAEFHDSDDHHTFKMLPRDRFRFRKASLDGD 177

QY 181 SMATRELTAFLPEEPFMRDVIATFLELDLRNKDGYVQVVEYIADLYSAPFGEEPA 240
 Db 178 LTATREFTAFLLPEEPFHHKEIVVLETIEDIKNGDGFVDQDEYIADMFSHEDNGPEP 237

QY 241 WVOTERQQRFRDLNKGHLDSGVGHVWVLPADOPPLVEANHLIHESDITDKDGR 300
 Db 238 WVLSERFQNFDRDLNKGKLDKDEIRHWILFQDYDHAQAEARHLVYESDKNKDEMLTKE 297

RESULT 3


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QY 7 VLLLLLLRHGA-----QGRPSDAGPHGGRVHQAAPLSDAPHDDAHGNGFYDHEAFLG 61
Db 3 VLLFGVLLAATALASHSSDPSND-GEHPKGEHDK-----KYDHEOFLG 46
QY 62 REVAKFEQDLTPESQARLGRIVDRMDRAGDGGWVSWLAELRAWIAHTQQRHIRDSVSA 121
Db 47 KDTAAEFDELTPEKSEKELAKLVKPMDD--ADSDGFIEENELKDLHNFQMRYVNDVDRT 104
QY 122 WDTYDTR--DGRVGWEELRNATYGHY-APGEEPHDVEDAETYKKMLARDERRFRVADQD 178
Db 105 WKNTKAEBKIVDGKIKWEDYRMVYGSADGAGEL-----SPEYAKMTARDEKRWADYD 159
QY 179 GDSMATREELTATLHPPEEPHMRDIVIAETLEDLRNKGQVGVVEEYIADLYSAEPGE- 237
Db 160 SNGALORTEYGCFCMHDFCDHNRVVAETVDDIDKNGKGSVDLDEYIGWYRPPDYPEL 219
QY 238 ---EPAWQTERQQRDFRDLNKGDLGDSVGHVWLPAPQDQPLVEANHLHESDTRDK 294
Db 220 NGKEPDWQVSEREMFKEHRDQDQGLKQNEEMRWIMPVGFDHAEAEARHLVGIADNDK 279
QY 295 GLSKAEILGNMFMVGSQATNYGEDLTRH 324
Db 280 GKULDEIVAHYDTFVGSQATDYEQLOKH 309

RESULT 5
156519
taipoxin-associated calcium binding protein-49 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 02-Aug-2002
C:Accession: I36519
R:Dodds, D.; Schillingen, A.K.; Lu, S.Y.; Perin, M.S.
A:Title: Novel reticular calcium binding protein is purified on taipoxin columns.
A:Reference number: 156519; PMID:95239201; PMID:7722520
A:Accession: 156519
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-318 <RES>
A:Cross-references: EMBL:U15734; NID:G606967; PIDN:AA80197.1; PID:G606968
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: calcium binding; EF hand
F:62-94/Domain: calmodulin repeat homology <EF1>
F:120-152/Domain: calmodulin repeat homology <EF2>
F:187-219/Domain: calmodulin repeat homology <EF3>
F:228-260/Domain: calmodulin repeat homology <EF4>
F:264-296/Domain: calmodulin repeat homology <EF5>

Query Match 26.9%; Score 476; DB 2; Length 318;
Best Local Similarity 35.2%; Pred. No. 1.6e-26;
Matches 117; Conservative 58; Mismatches 131; Indels 26; Gaps 8;

QY 4 RPSVLLLLLLLRHGAQGRPSDAGPHGGRVHQAAPLSDAPHDDAHGNGFYDHEAFLG-R 62
Db 6 RPAVLGELLLLLAAVAGASAKBELHYPOGE-HRA-----DYDREALGVQ 49
QY 63 EVAKFEQDLTPESQARLGRIVDRMDRAGDGGWVSWLAELRAWIAHTQQRHIRDSVSAW 122
Db 50 EDVDEVKLGHEEQRRQLSIKID--SDSDGFLTENLSQWISFKHYAMQEAQKF 107
QY 123 DTYDTRDGRVGEELRNATYGHYAPGEEPHDVEDA--ETYKKMLARDERRFRVADQDQ 180
Db 108 VEYDRNSDQTFWDEYNVQMYDVIDFDENTALDDTTEESFQHLKDKKFEKANQDSG 167
QY 181 SNATREELTATLHPPEEPHMRDIVIAETLEDLRNKGQVGVVEEYIADLYSAEP-GEPE 239
Db 168 PGLNLEEFATPEEPEVDYTFEVIQALEBHDKNGDGVFSLEELFGD-YRDRFTANEDP 226
QY 240 AWQTERQQRDFRDLNKGDLGDSVGHVWLPAPQDQPLVEANHLHESDTRDKGRLSK 299
Db 227 EMILVEKDRFVNDYKDSGRLPQDELLSWVFNQGIQAEALHLIDEMDLNSDKKLE 286
QY 300 AEILGNMFMVGSQATNYGEDLTR----HHDEL 328

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A:Gene: ERC-55
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: calcium binding; EF hand; endoplasmic reticulum
F:1-22/Domain: signal sequence #status predicted <SIG>
F:61-93/Domain: calmodulin repeat homology <EF1>
F:129-139/Domain: calmodulin repeat homology <EF2>
F:186-218/Domain: calmodulin repeat homology <EF3>
F:227-259/Domain: calmodulin repeat homology <EF4>
F:263-295/Domain: calmodulin repeat homology <EF5>
F:314-317/Region: endoplasmic reticulum retention signal

Query Match 25.88; Score 456.5; DB 2; Length 317;
Best Local Similarity 34.88; Pred. No. 3.8e-25;
Matches 116; Conservative 60; Mismatches 128; Indels 29; Gaps 9;
QY 4 RPSVLLLLHGHAGQKSPDAGPHGQGRVHQ-AFLSDAPDDHAGNQYDHEAFLG- 61
DB 6 RFAALGLLLC-----AAAAGAGAAELHYPLGRRSD-----YDEALLGV 47
QY 62 REVAKFQDLPPEESQARLGRIVDRMDRAGDGVWVSLAEALRAWIAHQRRHDSVSAA 121
DB 48 QEDVDYKVLGHEEQKRLQAIKKIDL--DSGFLTESELSSNIQMSFRHYAQEAQKQ 105
QY 122 WQYDTRDRGRVGEELRNATYGHYAPGEEHVEDA--EYKKMLARDERRFRVADQG 179
DB 106 FVEYDKNSDDTVTWDEYNIQMVDRIEDFEDNTALDDAEESEFRKLHLKRRKFEKANQDS 165
QY 180 DSMATREELTAFLHPEEPFMRDIVIAETLEDLRNKGQYVQVEEYIADLYSAEP-GEE 238
DB 166 GPGLSLEEFATFEPHEVDYMTFVIOEALAEHDKNGDGVSLSEFLGD-YRWDPANED 224
QY 239 PAWQTERQOFRDLNKGDLGSEVGHVWVLPAPADQPLVEANHLHESDTKDGRLS 298
DB 225 PEWLVKORFVNDYDKDNGRLDPQELLPVVVPNNQGTAAQEALHLIDEMDLNGDKKLS 284
QY 299 KAEILGNWNMFVGSQATNYGEDLTR---HDEL 328
DB 285 EEEILENPDILFTSEATDYGRQLHDDYFYHDEL 317

RESULT 8
T33849
hypothetical protein F08B6.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 16-Aug-2002
R:Le, T.T.; Scheet, P.; Kemp, K.
submitted to the EMBL Data Library, November 1998
A:Description: The sequence of C. elegans cosmid F08B6.
A:Reference number: 221423
A:Accession: T33849
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-313 <LET>
A:Cross-references: EMBL:AF106590; PIDN:AAC78237.1; GSPDB:GN00019; CESP:F08B6.3
A:Experimental source: strain Bristol N2; clone F08B6
C:Genetics:
A:Gene: CESP:F08B6.3
A:Map position: 1
A:Introns: 78/1; 112/3; 127/3; 161/1; 231/2
C:Superfamily: reticulocalbin; calmodulin repeat homology

Query Match 20.1%; Score 357; DB 2; Length 313;
Best Local Similarity 31.6%; Pred. No. 4.3e-18;
Matches 86; Conservative 51; Mismatches 101; Indels 34; Gaps 7;
QY 74 EESQARLGRIVDRMDRAGDGVWVSLAEALRAWIAHQRRHDSVSAAWDTYDTRDQ-- 131
DB 59 QESVERFAKALDT-----NNDGFVKSEILAWVSEYQKTVDRVRAERISELDENADGFL 113
QY 132 -----RVGWEELRNATYGHYAPGEEHVEDAETYYKKMLARDERRFRVADQG 178
DB 114 YFNTLFLSLVDRKHVSWEEYLDSP-----PDEELHNKEE-----ESLIAQDKMYFKQADE 165

QY 179 GDSMATREELTAFLHPEEPFMRDIVIAETLEDLRNKGQYVQVEEYIADLYSAEPGEE 238
DB 166 NDGKLNLEELASFLNPEHPHMPVLIATVLEKQDQNGDAIEKEFGL-DEQRGSE- 223
QY 239 PAWQTERQOFRDLNKGDLGSEVGHVWVLPAPADQPLVEANHLHESDTKDGRLS 298
DB 224 --WYKVEVERFTYVDKNGDKLAGDELTDWLLVDGTTAGSYAEASLLTNSDDDKDQGLS 281
QY 299 KAEILGNWNMFVGSQATNYGEDLTRH--HDEL 328
DB 282 VEEIVKHAFKAEAAQADHHLHPYSHDEL 313

RESULT 9
T09018
probable calcium-binding protein T27E11.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002
C:Accession: T09018
R:Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Ban-
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16533
A:Accession: T09018
A:Molecule type: DNA
A:Residues: 1-345 <BEV>
A:Cross-references: EMBL:AL078579; GSPDB:GN00062; ATSP:T27E11.30
A:Experimental source: cultivar Columbia; BAC clone T27E11
C:Genetics:
A:Gene: ATSP:T27E11.30
A:Map position: 4
A:Introns: 163/1; 197/2; 219/2; 304/3
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: EF hand

Query Match 12.1%; Score 214.5; DB 2; Length 345;
Best Local Similarity 27.4%; Pred. No. 6.3e-08;
Matches 82; Conservative 53; Mismatches 125; Indels 39; Gaps 12;
QY 56 HEAFGLR---EVAKE-----FDQLTPEE---SQARLGRIVDRMDRAGDGVWVSLAE 103
DB 60 HEKAGTKTVEAKKEKDMFEYFAOERLNTMRILKFLPLD-ASPRDGFVSLKELQ 118
QY 104 AWIAHQRRHDSVSAAWDTYDTRDGRVGEELRNATYGHYAPGEEHVEDAETYYK 163
DB 119 TWMMQOTEDNNVYRTAKELEQLDKDQGVTFEE-----YLPQFSKODIEKNEKGHG 170
QY 164 MLARDERRFRVADQDGSMAETRELTAFLEHPEEPH--MRDIVIAETLEDLRNKGQYVQ 221
DB 171 EAGWMEQFKNSDFDHNSLDIEEFNLFHEDSRNGDTQRWVLKERTMGDTNGDGKLE 230
QY 222 VEEYIADLYS-----AEPGEEPAWQTERQOFRDLNKGDLGSE---VGHWVLP 273
DB 231 YKEFVNAYEMKFAKEKEEDENVPTQLFAEM-DRDRDLVLADELPILOYLQPG 289
QY 274 ADOQPLVEANHLHESDTKDGRLSKAELLGNWNMFVGSQATNYGEDLTRH----HDEL 328
DB 290 EMSYAKFYSTFLCHAEDEKDKGLSLEELHHEVDVY--KAVHH-EDLDEDDYFDHDEL 345

RESULT 10
A42264
membrane-associated calcium-binding protein pfs40 - malaria parasite (Plasmodium fa-
C:Species: Plasmodium falciparum
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jun-2000
C:Accession: A42264
R:Rawlings, D.J.; Kaslow, D.C.
J. Biol. Chem. 267, 3976-3982, 1992
A:Title: A novel 40-kDa membrane-associated EF-hand calcium-binding protein in Plasmo-
A:Reference number: A42264; M0ID:92156141; PMID:1740445
A:Accession: A42264
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein

